

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 15:55:46 ; Search time 2581.68 Seconds  
(without alignments)  
3161.255 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

Sequence: 1 ATGCCCTGGACTGCTCCT.....CCCGGTGACCGTCCTAGGT 390

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg.hum.\*

31: em.htg.inv.\*

32: em.htg.other.\*

33: em.htgo.inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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1	340.4	87.3	435	9	HS285043	285043 H.sapiens I
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3	340.4	87.3	473	9	HUMIGLVS	M75139 Human Ig re
4	338.8	86.9	435	9	HS285033	285033 H.sapiens I
5	335.6	86.1	435	9	HS285358	285358 H.sapiens I
6	334	85.6	435	9	HS285035	285035 H.sapiens I
7	334	85.6	435	9	HS285297	285297 H.sapiens I
8	334	85.6	435	9	HS285355	285355 H.sapiens I
9	330.8	84.8	435	9	HS285038	285038 H.sapiens I
10	330.8	84.8	435	9	HS285362	285362 H.sapiens I
11	329.2	84.4	435	9	HS285034	285034 H.sapiens I
12	329.2	84.4	435	9	HS285360	285360 H.sapiens I
13	329.2	84.4	435	9	HS285364	285364 H.sapiens I
14	327.6	84.0	435	9	HS285032	285032 H.sapiens I
15	327.6	84.0	453	9	HSU43772	U43772 Human Immun
16	326	83.6	435	9	HS285029	285029 H.sapiens I
17	325.8	83.5	894	9	BC018749	BC018749 Homo sapi
18	324	83.1	375	9	HS285091	285091 H.sapiens I
19	322.8	82.8	435	9	HS285295	285295 H.sapiens I
20	322.8	82.8	435	9	HS285303	285303 H.sapiens I
21	322.8	82.8	450	9	HSWLRG	X62125 H.sapiens I
22	321.2	82.4	435	9	HS284919	284919 H.sapiens I
23	321.2	82.4	435	9	HS285036	285036 H.sapiens I
24	321.2	82.4	435	9	HS285302	285302 H.sapiens I
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34	316.4	81.1	435	9	HS285030	285030 H.sapiens I
35	316.4	81.1	435	9	HS285040	285040 H.sapiens I
36	316.2	81.1	435	9	HS285031	285031 H.sapiens I
37	316.2	81.1	435	9	HS285300	285300 H.sapiens I
38	314.8	80.7	435	9	HS284926	284926 H.sapiens I
39	314.8	80.7	435	9	HS285363	285363 H.sapiens I
40	313.6	80.4	360	9	HS285359	285359 H.sapiens I
41	313.6	80.4	360	9	HS285179	285179 H.sapiens I
42	313.6	80.4	360	9	HS285183	285183 H.sapiens I
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44	313	80.3	435	9	HS285301	285301 H.sapiens I
45	313	80.3	435	9	HS285357	285357 H.sapiens I

#### ALIGNMENTS

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HS285043

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

HS285043 435 bp DNA linear PRI 06-FEB-1997  
H.sapiens Ig lambda light chain variable region gene  
(24-17TIIIIH34) rearranged; Ig-Light-Lambda; VLambda.

285043.1 GI:1834754

antigen receptor; immunoglobulin light chain;  
immunoglobulin superfamily; rearranged; variable region.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)

Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

XXXXThe Creation of Diversity in the Human Immunoglobulin V Lambda

Repertoire

J. Mol. Biol. In press

2 (bases 1 to 435)

Ignatovich,O.

Direct Submission

Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein

Engineering, Hills Road, Cambridge CB2 2QH, UK

[illegible]

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ACCESSION M75139
VERSION M75139.1 GI:186154
KEYWORDS C-region; J-region; V-region; immunoglobulin; immunoglobulin
lambda; immunoglobulin light chain; variable region subgroup II.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Paul, E., Livneh, A., Manheimer-Lory, A.J. and Diamond, B.
Characterization of the human Ig lambda II gene family and
analysis of V lambda II and C lambda polymorphism in systemic lupus
erythematosus [published erratum appears in J Immunol 1993 Apr
15;150(8 pt 1):3668]
JOURNAL J. Immunol. 147 (8), 2771-2776 (1991)
MEDLINE 92013092
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QY 121 TGCACCTGGAACACGATGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
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Db 210 CCAGCTAAGCCCCCAACTCATGATTTATGATGTCGCTAAGCGGCTCAGGGTCTCT 269
QY 241 GATCGCTTCTCTGGCTCCCAAGCTGGCAACACGCGCTCCCTGACCATCTCTCTGG 300
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Db 330 GCTGAGGACGAGGCTGATTTACTGTTTATATATACAAACAGTAGACTTTGTTATTC 389
QY 361 GGAAGAGGACCGGTTGACCTCCCTAGCT 390
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Db 390 GCGGAGGACCAAGCTGACCGCTCCTAGGT 419
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DEFINITION H.sapiens Ig lambda light chain variable region gene
(24-07ITIB176); rearranged; Ig-Light-Lambda; V Lambda.
ACCESSION 285033
VERSION 285033.1 GI:1834744
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Ignatovich, O., Tomlinson, I.M., Jones, P.T. and Winter, G.
XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Repertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich, O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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Db 361 GCGGAGGACCAAGCTGACCGTCTTAGGT 390

## RESULT 5

HS285358  
LOCUS  
DEFINITION H.sapiens Ig lambda light chain variable region gene (25-28SWID60)  
rearranged; Ig-Lambda; VLambda.

ACCESSION 285358

VERSION 285358.1 GI:1835069  
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;  
immunoglobulin superfamily; rearranged; variable region.

## SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 435)

AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda

JOURNAL Repertoire

REFERENCE 2 (bases 1 to 435)

AUTHORS Ignatovich,O.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein

Engineering, Hills Road, Cambridge CB2 2QH, UK

FEATURES

source

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RESULT 6

HS285035

LOCUS

DEFINITION H.sapiens Ig lambda light chain variable region gene

(24-09ITIIIC195) rearranged; Ig-Lambda; VLambda.

ACCESSION 285035

VERSION 285035.1 GI:1834746

KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;

immunoglobulin superfamily; rearranged; variable region.

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 435)

AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.

TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda

JOURNAL Repertoire

REFERENCE 2 (bases 1 to 435)

AUTHORS Ignatovich,O.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein

Engineering, Hills Road, Cambridge CB2 2QH, UK

FEATURES

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Db	301		
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DEFINITION	H.sapiens Ig lambda light chain variable region gene (25-23SWIB16) rearranged; Ig-Light-Lambda; VLambda.		
ACCESSION	285355		
VERSION	285355.1	GI:1835066	
KEYWORDS	antigen receptor; immunoglobulin; immunoglobulin light chain; immunoglobulin superfamily; rearranged; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 435)		
TITLE	Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.		
JOURNAL	XXXXThe Creation of Diversity in the Human Immunoglobulin V Lambda Repertoire		
REFERENCE	J. Mol. Biol. In press		
AUTHORS	2 (bases 1 to 435)		
TITLE	Ignatovich,O.		
JOURNAL	Direct Submission		
FEATURES	Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, UK		
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ACCESSION Z85038
VERSION 285038.1 GI:1834749
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immunoglobulin superfamily; rearranged; variable region.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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Matches 353; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGGCTGGACTCTGCTCTCTGCTCACCCTCCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
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Db 181 CCAGCAAAAGCCCCCAACTCATGATTATGAGTGCTACTAAGCGGCCCTCAGGGGTCTCCT 240
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RESULT 10
HSZ85362 HSZ85362 435 bp DNA linear PRI 06-FEB-1997
LOCUS H.sapiens Ig lambda light chain variable region gene
DEFINITION (25-33SWIIE224) rearranged; Ig-Lambda; VLambda.
ACCESSION Z85362
VERSION 285362.1 GI:1835073
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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Matches 353; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 ATGGGCTGGACTCTGCTCTCTGCTCACCCTCCCTCACTCAGGGGCACAGGATCCTGGGCTCAG 60
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QY 301 GCTGAGGAGCGGCTGATTATTACTGTTTTCATATACACAGGAGTCTCTGGGTCTTCTTTC 360
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(24-08ITIIC194) rearranged; Ig-Light-Lambda; VLambda.
ACCESSION 285034
VERSION 285034.1 GI:1834745
KEYWORDS antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
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QY 1 ATGGGCTGGACTCTGCTCTGCTCAACCTCCCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
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DB 361 GGAAGAGGACCGGTTGACCGTCTCTAGGT 390

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VERSION 285360.1 GI:1835071
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
TITLE XXThe Creation of Diversity in the Human Immunoglobulin V Lambda
Reertoire
JOURNAL J. Mol. Biol. In press
REFERENCE 2 (bases 1 to 435)
AUTHORS Ignatovich,O.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
FEATURES
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Matches 352; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1 ATGGGCTGGACTCTGCTCTGCTCAACCTCCCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
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ACCESSION Z85032.1 GI:1834743				
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KEYWORDS immunoglobulin superfamily; immunoglobulin; immunoglobulin light chain;				
SOURCE human,				
ORGANISM Homo sapiens				
REFERENCE 1 (bases 1 to 435)				
AUTHORS Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.				
TITLE XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda Repertoire				
JOURNAL J. Mol. Biol. In press				
REFERENCE 2 (bases 1 to 435)				
AUTHORS Ignatovich,O.				
TITLE Direct Submission				
JOURNAL Submitted (06-FEB-1997) Ignatovich O., MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, UK				
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Db 61 TCTGCCCTGACTCAGCTCCCTCGGTCTGGTCTCCCTGGACAGTCGATCAACCATCTCC 120
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DEFINITION Human immunoglobulin light chain variable region mRNA, cell line
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VERSION     U43772.1 GI:1353829
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ORGANISM    human.
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REFERENCE   1 (bases 1 to 453)
AUTHORS     Boucher,G., Broly,H. and Lemieux,R.
TITLE       Restricted Use of Cationic Germline VH Gene Segments in Human Rh(D)
JOURNAL     Red Cell Antibodies
REFERENCE   2 (bases 1 to 453)
AUTHORS     Boucher,G.
TITLE       Direct Submission
JOURNAL     Submitted (21-DEC-1995) Gerard Boucher, Research and Development,
             The Canadian Red Cross Society, Transfusion Center of Quebec, 2535
             Laurier Boulevard, Ste-Foy, Quebec G1V 4M3, Canada
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Matches 351; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 1 ATGGCCCTGACTGTGCTCGCTCGTCACCCCTCCTCACTCAGGGCACAGGATCCTCTGGGCTCAG 60
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Job time: 6857 sec
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 15:51:41 ; Search time 3874.81 Seconds  
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Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: gb\_est2: \*  
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16: em\_gss\_vrt: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	329.2	84.4	686	10	BF975970 602115633
6	329.2	84.4	716	9	BF975970 602115633
7	329.2	84.4	767	9	BF975970 602115633
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#### ALIGNMENTS

#### RESULT 1

BF975970

LOCUS

DEFINITION

BF975970

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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mRNA sequence.  
BF975970  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLC1211 row: c column: 19  
High quality sequence stop: 759.  
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for average insert size 1.8kb. Library constructed by Ling

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLC1211 row: c column: 19  
High quality sequence stop: 759.  
Location/Qualifiers  
1. 880  
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/db\_xref="taxon:9606"  
/clone="IMAGE:4337226"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
Site:2: EcoRI; cDNA made by oligo-dt priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

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BASE COUNT      200 a      283 c      219 g      178 t
ORIGIN

Query Match      86.9%; Score 338.8; DB 10; Length 880;
Best Local Similarity 91.8%; Pred. No. 2.2e-80;
Matches 358; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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QY	61	TCCTGCCCGGACTCAGCCTCCCTCTGTGTCCTGGGTCTCCTGGACAGTCGGTCACCATCTCC	120
Db	93	TCCTGGCCTGACTCAGCGTCGCTCCGTCTCTGGGTCTCTGGACAGTCGATCACCATCTCC	152
QY	121	TGCACCTGGAAACCAGGATCAGCTTGGTGGTTATAACTATGTCTCTGGTACCACACACCAC	180
Db	153	TGCACCTGGAAACCAGAGTCAGCTTGGTGGTTATAACTATGTCTCTGGTCCCACACACAC	212
QY	181	CCAGGCAAGCCCCCAAACTCATGATTTATGATGTGCTTAAGCGGGCCTCAGGGGTCTCT	240
Db	213	CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCAAGTAATCGGCCCTCAGGGGTCTCT	272
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QY	361	GGAAGAGGGACCCGGTTTGACCGTCTCTAGGT	390
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RESULT	2
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LOCUS	
DEFINITION	843 bp mRNA linear EST 15-MAY-2001 602715633F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855593 , mRNA sequence.
ACCESSION	BG756493
VERSION	BG756493.1 GI:14067146
KEYWORDS	EST.
SOURCE	human.

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 843)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov  
Tissue procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA library preparation: Ling Hong/Rubin Laboratory  
CDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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http://image.fiml.gov
plate: LLCM1705 row: b column: 10
High quality sequence stop: 838.

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FEATURES
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1. .843
Location/Qualifiers
"sgn" quality sequence stop: 0.50
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/db_xref="taxon:9606"
/clone="IMAGE:4855593"
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/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
187 a 278 c 217 g 161 t

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BASE COUNT      187 a      278 c      217 g      161 t
ORIGIN
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Best Local Similarity 91.0%;      pred. No. 4.1e-79;
Matches 355;      Conservative      0;      Mismatches 35;      Indels 0;      Gaps 0;

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Qy	61	TCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC	120
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Qy	361	GGAAAGAGGGACCCGGTTGACCGCTCTTAGGT	390
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RESULT	3	
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LOCUS		
DEFINITION		
ACCESSION	BI820758	787 bp
VERSION	BI820758	mRNA
KEYWORDS	BI820758.1	linear
SOURCE	EST.	
	human.	
	GI:15932308	
	mRNA sequence.	
	603034354F1	
	NIH_MGC_115	
	Homo sapiens	
	cdna clone IMAGE:5175684	
	5',	
		EST 04-OCT-2001

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 787)  
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>  
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)  
UNPUBLISHED (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT

CONTACT: Robert Srauspey, Ph.D.  
Email: cgaaps-r@mail.nih.gov  
Tissue procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at:







Qy	301	GCTGAGGACGAGGCTGATTTACTGTGTTCATATACACCACTAGACATTTCTTTATTC	360
Db	329	GCTGAGGACGAGGCTGATTTACTGTGTTCATATACACCACTAGACATTTCTTTATTC	388
Qy	361	GGAGAGGAGCCCGTTGACCGTCTAGGT	390
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RESULT	8		
LOCUS	BG758901		
DEFINITION	602713013F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853450 5', mRNA linear EST 15-MAY-2001		
ACCESSION	BG758901		
VERSION	1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates: Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L16M1699 row: 1 column: 03 High quality sequence stop: 786.		
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	/tissue_type="primary B-cells from tonsils (cell line)"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
BASE COUNT	176 a 261 c 206 g		
ORIGIN	143 t		
Query Match	84.4%	Score 329.2; DB 10; Length 786;	
Best Local Similarity	90.3%	Pred. No. 7.7e-78;	
Matches	352; Conservative	0; Mismatches 38; Indels 0; Gaps 0;	
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Db	32	ATGGCCCTGGGCTCTGCTCCCTCTCACCTCTCTACTCAGGGCAGGAGTCTGGGCTCAG	91
Qy	61	TCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCGGACAGTCCGGTCAACATCTCC	120
Db	92	TCTGCCCTGACTCAGCCTCCCTCCCGGCTCCGGTCTCTCGGACAGTCACTCACTCTCC	151
Qy	121	TGCACTGGAAACCAACGAGTACGCTGGTGGTGGTTATTAACATATGTCTCTGGTACCAACACAC	180
Db	152	TGCACTGGAAACCAACGAGTACGCTGGTGGTGGTATTAACATATGTCTCTGGTACCAACAGCAG	211







JOURNAL with those of corresponding noncancerous liver  
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
COMMENT 21625106

Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922

Email: hanzgchc.sh.cn  
This clone is available at CHGC in Shanghai.

# FEATURES

Location/Qualifiers  
1..710

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="GKCGWE01"  
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/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 147 a 239 c 182 g 142 t

Query Match 84.0%; Score 327.6; DB 9; Length 710;

Best Local Similarity 90.0%; Pred. No. 2e-77; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCGTGGACTCTGCTCTCGTCAACCTCCCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
DB 29 ATGGCGTGGGCTCTGCTATTCCTCAACCTCCCTCACTCAGGGCACAGGATCCTGGGCTCAG 88
QY 61 TCTGCCCCGACTCAGCCCTCCCTCTGTGTGGTCTCTGGAGTTCGCTCACCATTCTCC 120
DB 89 TCTGCCCCGACTCAGCCCTCCCTCTGTGTGGTCTCTGGAGTTCGCTCACCATTCTCC 148
QY 121 TGCACCTGGACAGCAGTACGCTTGGTGTATTAATCTATGCTCTCTGGTACCAACAC 180
DB 149 TGCACCTGGACAGCAGTACGCTTGGTGTATTAATCTATGCTCTCTGGTACCAACAC 208
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DB 209 CCAGGCAAGCCCCCAAACTCATGATTTATGCTGCTAAGCGGCTCAGGGGTCTCT 268
QY 241 GATCGCTTCTCTGGGTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
DB 269 AATCGCTTCTCTGGGTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 328
QY 301 GCTGAGGAGGAGGCTGATTTACTGTTTCATATACACAGTAGACATTTGTTATTC 360
DB 329 GCTGAGGAGGAGGCTGATTTACTGACGCTCATATACAGCGGCACTCCGGTGTTC 388
QY 361 GGAAGAGGAGGAGGCTGACCGTCTCTAGT 390
DB 389 GCGCAGGAGGAGGCTGACCGTCTCTAGT 418

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# RESULT 15

LOCUS AV699040 751 bp mRNA linear EST 16-JAN-2002  
DEFINITION AV699040 GK Homo sapiens cDNA clone GKCGX207 5', mRNA sequence.

ACCESSION AV699040

VERSION AV699040.1 GI:10301011

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 751)

AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,

Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,

Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,  
Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level  
by comparing gene expression profiles of hepatocellular carcinoma  
with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

# JOURNAL

# MEDLINE

# COMMENT

Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922

Email: hanzgchc.sh.cn

This clone is available at CHGC in Shanghai.

# FEATURES

Location/Qualifiers

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/db\_xref="taxon:9606"  
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/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 166 a 241 c 201 g 143 t

Query Match 84.0%; Score 327.6; DB 9; Length 751;

Best Local Similarity 90.0%; Pred. No. 2e-77; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCGTGGACTCTGCTCTCGTCAACCTCCCTCACTCAGGGCACAGGATCCTGGGCTCAG 60
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QY 61 TCTGCCCCGACTCAGCCCTCCCTCTGTGTGGTCTCTGGAGTTCGCTCACCATTCTCC 120
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QY 121 TGCACCTGGACAGCAGTACGCTTGGTGTATTAATCTATGCTCTCTGGTACCAACAC 180
DB 131 TGCACCTGGACAGCAGTACGCTTGGTGTATTAATCTATGCTCTCTGGTACCAACAC 190
QY 181 CCAGGCAAGCCCCCAAACTCATGATTTATGCTGCTAAGCGGCTCAGGGGTCTCT 240
DB 191 CCAGGCAAGCCCCCAAACTCATGATTTATGCTGCTAAGCGGCTCAGGGGTCTCT 250
QY 241 GATCGCTTCTCTGGGTCCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
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QY 301 GCTGAGGAGGAGGCTGATTTACTGTTTCATATACACAGTAGACATTTGTTATTC 360
DB 311 GCTGAGGAGGAGGCTGATTTACTGACGCTCATATACAGCGGCACTCCGGTGTTC 370
QY 361 GGAAGAGGAGGAGGCTGACCGTCTCTAGT 390
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Job time: 4504 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 16:01:56 ; Search time 488.47 Seconds  
(without alignments)  
1370.804 Million cell updates/sec

Title: US-09-019-441-1  
Perfect score: 390  
Sequence: 1 ATGGCTGGACTGCTCTCT.....CCCGTTGACCGTCTAGGT 390

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	AAV33307	Anti-human CD23 6G
2	321.2	82.4	891	AA66528	Human immune syste
3	319.6	81.9	902	AAQ35100	Antibody D lambda
4	316.4	81.1	889	AA377073	DNA encoding novel
5	313.6	80.4	763	AA583480	DNA encoding novel
6	310	79.5	448	AA577070	DNA encoding novel
7	307.2	78.8	7528	AA330316	Bicistronic idioxy
8	306.8	78.7	756	AA583477	DNA encoding novel
9	306.8	78.7	866	AA587037	DNA encoding novel

10	305.2	78.3	453	23	AA577071	DNA encoding novel
11	303.6	77.8	637	23	AA577074	DNA encoding novel
12	298.8	76.6	783	23	AA583483	DNA encoding novel
13	298.6	76.6	414	23	AA577069	DNA encoding novel
14	297	76.2	863	23	AA583485	DNA encoding novel
15	295.6	75.8	876	23	AA583478	DNA encoding novel
16	295.2	75.7	548	21	AA68957	Human ovarian carc
17	292.4	75.0	351	22	AA168755	Human autoantibody
18	284.6	73.0	628	14	AAQ36134	MH4H7 MAB light ch
19	284.6	73.0	1044	12	AAQ12840	Variable region of
20	284.4	72.9	351	22	AA168765	Human autoantibody
21	281.2	72.1	747	21	AA67868	Recombinant human
22	280.8	72.0	333	22	AAH42401	Nucleotide sequenc
23	280.8	72.0	333	22	AAH42407	Nucleotide sequenc
24	278.4	71.4	9071	13	AAQ22491	Human U266 lambda
25	278.4	71.4	9071	13	AAQ22370	U266-Lambda gene a
26	275.4	70.6	333	17	AA10327	Human anti-Pseudom
27	275.4	70.6	333	20	AA231655	Coding sequence fo
28	274.8	70.5	351	22	AA168759	Human autoantibody
29	273.8	70.2	333	20	AA231654	Coding sequence fo
30	271.2	69.5	729	22	AAH47763	Anti-hEDRF antibod
31	270.8	69.4	330	22	AA503477	DNA encoding anti-
32	269.2	69.0	330	22	AA503520	DNA encoding anti-
33	269	69.0	342	21	AA62337	DNA encoding a var
34	265.8	68.2	333	15	AAQ55659	Monoclonal antibod
35	263	67.4	777	23	AA577072	DNA encoding novel
36	261.8	67.1	360	24	ABA94221	EBV transformant a
37	258	66.2	336	22	AA503509	DNA encoding anti-
38	258	66.2	529	23	AA579448	DNA encoding novel
39	249.2	63.9	717	22	AAF58707	Huntingtin intrabo
40	248.4	63.7	327	22	AAF58706	Huntingtin minimal
41	246.8	63.3	747	22	AAH76382	Nucleotide sequenc
42	246.6	63.2	375	20	AAV72228	Human anti-GPIIb/I
43	246.4	63.2	336	22	AAH42391	Nucleotide sequenc
44	244.4	62.7	402	22	AAH35419	Human colon cancer
45	241.8	62.0	482	22	ABA58301	Human foetal liver

ALIGNMENTS

RESULT 1  
ID AAV33307 standard; DNA; 390 BP.

AAV33307;

18-NOV-1998 (first entry)

Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA.  
Anti-human CD23 6G5 monoclonal antibody; light chain variable region;  
human CD23; Ig; FcεRII/CD23; gamma-1 constant region;  
gamma-3 constant region; allergy; inflammation; autoimmune disease;  
allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.

Macaca fascicularis

Key Location/Qualifiers

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/\*note= "CDS does not contain a stop codon"  
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FT /\*note= "encodes CDR 1 region"  
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FT /\*tag= e

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FT 328..357 /*tag= f
FT /note= "encodes CDR 3 region"
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PN WO9837099-A1.
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XX 27-AUG-1998.
XX
XX 17-FEB-1998; 98WO-US02253.
XX
XX 05-FEB-1998; 98US-0803085.
XX 20-FEB-1997; 97US-0803085.
XX
XX (IDEC-) IDEC PHARM CORP.
XX (SEK ) SEIKAGAKU CORP.
XX
XX Kloetzer WS, Nakamura T, Reff ME;
XX
XX WPI; 1998-467495/40.
XX P-PSDB; AAW70377.
XX
XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE
XX expression to treat or prevent allergic, inflammatory and
XX auto:immune conditions
XX
XX Example 1; Pages 102-104; 146pp: English.
XX
XX The present sequence represents a DNA sequence encoding the light
XX chain variable region of primate monoclonal antibody anti-human CD23 6G5.
XX The invention provides primate monoclonal antibodies which specifically
XX bind human CD23, the low affinity receptor for IgE (FcεRI/CD23),
XX and comprise either a human gamma-1 or human gamma-3 constant region
XX that binds to human Fc gamma receptors and inhibits IgE expression.
XX The monoclonal antibodies of the invention are claimed to be useful
XX for inhibiting induced IgE production for treating or preventing
XX allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
XX conjunctivitis, autoimmune haemolytic anaemia, etc.
XX
XX Sequence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;

Query Match 100.0%; Score 390; DB 19; Length 390;
Best Local Similarity 100.0%; Pred. NO. 1.6e-109;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTGTCACCCCTCCTCAGGCGACAGGATCCTGGGCTCAG 60
DB 1 atggctggactctgtctctgtccctcactcagggcacaggatcctgggctcag 60

QY 61 TCTGCCCGGACTCAGCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCAACATCTCC 120
DB 61 tctgccccgactcagctccctctgtctgtggtctctcctggacagtcggtcaccatctcc 120

QY 121 TGCACCTGGAAACGACGATGACGTTGGTGGTTAATACTATGTCCTCGGTACCAACACCAC 180
DB 121 tgcactggaaacgacgacgttggtgggttataactatgtctcctgggtacccaaccac 180

QY 181 CCAGGCAAGGCCCCAAACTCATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT 240
DB 181 ccaggcaagggccccaaactcatgatttataactatgtctcctgggtacccaaccac 240

QY 241 GATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
DB 241 gatcgcttctctggctcccaagtctggcaacacgggctccctgacctctctgggctccag 300

QY 301 GCTGAGCAGCAGCTGATTATTACTGTTTTCATATACACAGTAGACATTTGTTATTTC 360
DB 301 gctgagcagcagctgattattactgttttcataatacaacagtagacatttggttatttc 360

QY 361 GGAAGAGGACCGGTTGACCGTCTAGGT 390
DB 361 ggaagaggacccgggttgaccgtctcagggt 390
```

```
RESULT 2
AAC66528
ID AAC66528 standard; cDNA; 891 BP.
XX
AC AAC66528;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human immune system associated protein HISAP-10 coding sequence.
XX
KW Human: immune system associated protein; HISAP-10; immune disorder;
XX infection; autoimmune disease; cancer; ss.
XX
OS Homo sapiens.
XX
PN US6135941-A.
XX
PD 24-OCT-2000.
XX
PF 27-MAR-1998; 98US-0049672.
XX
PR 27-MAR-1998; 98US-0049672.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
XX Hillman JL, Au-Young J;
XX
DR WPI; 2001-030926/04.
DR P-PSDB; AAB63212.
XX
XX New human immune system associated proteins (HISAP) and polynucleotides
XX encoding the HISAP, useful for diagnosing, treating or preventing
XX immune or cell proliferative disorders or infections
XX
XX Claim 3; Column 87-90; 54pp: English.
XX
XX The present invention provides the coding and protein sequences for a
XX number of human immune system associated proteins (HISAPs). These can be
XX used in the diagnosis and treatment of various autoimmune disorders,
XX infections and cell proliferation diseases. The diseases include AIDS,
XX adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
XX Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
XX gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
XX erythematosus, arteriosclerosis, cirrhosis and cancer.
XX
XX Sequence 891 BP; 207 A; 287 C; 222 G; 175 T; 0 other;

Query Match 82.4%; Score 321.2; DB 22; Length 891;
Best Local Similarity 89.0%; Pred. No. 2.4e-88;
Matches 347; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGGCTGGACTCTGCTCTGTCACCCCTCCTCAGGCGACAGGATCCTGGGCTCAG 60
DB 34 atggctggactctgtctctgtctcctcactcagggcacagggtcctgggcccag 93

QY 61 TCTGCCCGGACTCAGCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCAACATCTCC 120
DB 94 tctgccccgactcagctccctctgtctgtggtctcctggacagtcgacatcctcc 153

QY 121 TGCACCTGGAAACGACGATGACGTTGGTGGTTAATACTATGTCCTCGGTACCAACACCAC 180
DB 154 tgcactggaaacgacgacgttggtgggttataactatgtctcctcgttaccacagtc 213

QY 181 CCAGGCAAGGCCCCAAACTCATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT 240
DB 214 ccaggcaagggccccaaactcatgatttataactatgtcgtcgtcctcaggggttct 273

QY 241 GATCGCTTCTCTGGCTCCCAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCAG 300
DB 241 gatcgcttctctggctcccaagtctggcaacacgggctccctgacctctctgggctccag 300
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PN W0200109303-A2.  
XX 08-FEB-2001.  
XX 31-JUL-2000; 2000WO-US20679.  
XX 30-JUL-1999; 99US-0146170.  
XX (VICA-) VICAL INC.  
XX Hermanson GG;  
XX WPI; 2001-123319/13.  
XX Immunogenic compositions comprising Flt-3 ligand encoding  
PT polynucleotide and one or more antigen, or cytokine encoding  
PT polynucleotides, useful for suppressing tumour growth and for treating  
PT autoimmune diseases (e.g. rheumatoid arthritis) -  
XX Example 2; Page 101-106; 149pp; English.  
XX The present sequence is that of patient-specific bicistronic  
CC chimeric idiotype VRI642 (Plasmid VAXID), which is used to treat  
CC B-cell lymphoma patients. The plasmid includes the cytomegalovirus  
CC immediate-early promoter, enhancer and 5' untranslated sequences,  
CC driving the expression of mouse-human chimeric immunoglobulin  
CC light and heavy chain sequences. The human light and heavy chain  
CC variable regions are derived from B-cell lymphoma cell line RAMOS.  
CC The transcriptional terminator region includes polyA and termination  
CC signals from the bovine growth hormone gene. According to the  
CC invention, co-administration of VRI642 with a plasmid (see AAF30314)  
CC encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a  
CC means of treating a patient with B-cell lymphoma.  
XX Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;

Query Match 78.8%; Score 307.2; DB 22; Length 7528;  
Best Local Similarity 88.3%; Pred. No. 1.1e-83;  
Matches 346; Conservative 0; Mismatches 43; Indels 3; Gaps 1;  
QY 1 ATGGCTGGAGCTGCTCCCTCGTCACCTCTCCTACATCAGGCGACAGATCCTGGGCTCAG 60  
Db 6 atggcctgggctctgctgctccacccctcactcagggcagggctcctgggcccag 65  
QY 61 TCTGCCCGGACTCAGCCTCCCTCTGTCTGTGGGTCTCCTGGACAGTCGGTCACTCTCC 120  
Db 66 tctgccctgactcagctgctcctgctgtctgtctctgagcagtcgataccatctcc 125  
QY 121 TGCACTGGAAACCGAGTACGTTGGTGGTTAATACTATCTCTCTGGTACCAACACCAC 180  
Db 126 tgcactggaaccagcagtgatgtgggagttataaccctgtctcctggtaccacaacac 185  
QY 181 CCAGGCAACGCCCCAAACATCATGATTATGATCTCGCTAAGCGGCGCTCAGGGTCTCT 240  
Db 186 ccagggcaagcccccaaacatcagttatgattgagtcagtaatcgccctcagggattct 245  
QY 241 GATCGGTTCTCTGGCTCCAAAGTCTGGCAACACGCGCTCCTGACCATCTCTGGGCTCCAG 300  
Db 246 aatcgcttctctgctccaaagtctggaacacagcctcctcctgacctctctgggctccag 305  
QY 301 GCTGAGACGAGGCTGATTATTAATGTTGTTATATACACACAGTAGCA---CTTTGTTA 357  
Db 306 gctgacgacgagggctgattattactgcaacctatatacaaacgacagcaattctcaggta 365  
QY 358 TTCGGAAGGGGACCGGTTGACCGTCTAGG 389  
Db 366 ttcggcggaggcccaagctgacctctcctagg 397

RESULT 8  
AAS83477  
ID AAS83477 standard; cDNA; 756 BP.

XX AAS83477;  
AC 13-FEB-2002 (first entry)  
XX DNA encoding novel human diagnostic protein #19281.  
DT Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX W0200175067-A2.  
PN 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
PD 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
PR (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
PI WPI; 2001-639362/73.  
XX P-PSDB; ABG19290.  
DR New isolated polynucleotide and encoded polypeptides, useful in  
XX diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX Claim 1; SEQ ID NO 19281; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX Sequence 756 BP; 161 A; 240 C; 197 G; 158 T; 0 other;

Query Match 78.7%; Score 306.8; DB 23; Length 756;  
Best Local Similarity 86.7%; Pred. No. 5.9e-84;  
Matches 338; Conservative 0; Mismatches 52; Indels 0; Gaps 0;  
QY 1 ATGGCTGGAGCTGCTCCCTCGTCACCTCTCCTACATCAGGCGACAGATCCTGGGCTCAG 60  
Db 1 atggcctggactctgctattctccaccctcactcagggcagggctcctggggcccag 60  
QY 61 TCTGCCCGGACTCAGCCTCCCTCTGTCTGTGGGTCTCTCGGTCCTCGGTCAGCATCTCC 120  
Db 61 tctgccctgactcagcctgctcctcctgctgtctgggtctcctggagacagtcgataccatctcc 120  
QY 121 TGCACTGGAAACCGAGTACGTTGGTGGTTAATACTATCTCTCTGGTACCAACACCAC 180

Db 121 tgcattggcaccagcagtgacattggtgcttatttatttcttcttctggtaccagcaatat 180  
QY 181 CCAGGCAAAAGCCCCCAACTCATGATTTATGATGCTGCTTAAGCGGGCCTCAGGGGTCTCT 240  
Db 181 ccaggcaaaagcccaactcttatttatttatttgcagtggtcgccctcagggatttct 240  
QY 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300  
Db 241 agtcgcttctctggtcccaagctggcaacacggctccctgacctatctctgggtccag 300  
QY 301 GCTGAGCAGGAGCTGATTTACTTCTTCTTATATACAAACAGTAGCAGTCTGTTATTC 360  
Db 301 gctgaggaagcaggtgattatttatttgcgttctcatatgcaagaagtagcaggtagcttcc 360  
QY 361 GGAAGAGGACCGGTTGACCTCTAGGT 390  
Db 361 ggcggaggaccagcagtgacctctcttgg 390

## RESULT 9

AAS87037  
ID AAS87037 standard; cDNA; 866 BP.  
AC AAS87037;  
DT 13-FEB-2002 (first entry)  
DE DNA encoding novel human diagnostic protein #22841.  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
XX 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX P-PSDB; ABG22850.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity -  
XX  
XX Claim 1: SEQ ID No 22841; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 866 BP; 200 A; 274 C; 213 G; 179 T; 0 other;

Query Match 78.7%; Score 306.8; DB 23; Length 866;  
Best Local Similarity 86.7%; Pred. No. 6.2e-84;  
Matches 338; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 ATGGCGCTGAGCTCTGCTCTGCTACCCCTCTCACTCAGGCGACAGATCTCGGGCTCAG 60  
Db 1 atggcgtgactctgtctattctccctcctcactcagggcacagggctcctgggccag 60  
QY 61 TCTGCCCGGACTCAGCCTCCCTCTGCTGCTGGTCTCTGGGACAGTCTGCTCACCATCTCC 120  
Db 61 tctgcccgtgactcagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 120  
QY 121 TGCATGGAACACGAGGATGACGTTGGTGTATATACTATGCTCTCTGTTACCAACACCAC 180  
Db 121 tgcatggcaccagcagtgacattggtgtatttatttctctctctggtaccagcaatat 180  
QY 181 CCAGGCAAAAGCCCCCAACTCATGATTTATGATGCTGCTTAAGCGGGCCTCAGGGGTCTCT 240  
Db 181 ccaggcaaaagcccaactcttatttatttatttatttatttatttatttatttatttattt 240  
QY 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300  
Db 241 agtcgcttctctggtcccaagctggcaacacggctccctcctcctcctcctcctcctcctc 300  
QY 301 GCTGAGCAGGAGCTGATTTACTTCTTATATACAAACAGTAGCAGTCTGTTATTC 360  
Db 301 gctgaggaagcaggtgattatttatttgcgttctcatatgcaagaagtagcaggtagcttcc 360  
QY 361 GGAAGAGGACCGGTTGACCTCTAGGT 390  
Db 361 ggcggaggaccagcagtgacctctcttgg 390

## RESULT 10

AAS77071  
ID AAS77071 standard; cDNA; 453 BP.  
XX AAS77071;  
XX AAS77071;  
DT 13-FEB-2002 (first entry)  
XX DNA encoding novel human diagnostic protein #12875.  
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX Homo sapiens.  
XX WO200175067-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US08631.  
XX 31-MAR-2000; 2000US-0540217.  
XX 23-AUG-2000; 2000US-0649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI: 2001-639362/73.  
XX P-PSDB; ABG12884.













GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:59:10 ; Search time 662.78 Seconds  
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1896.375 Million cell updates/sec

Title: US-09-019-441-1

Perfect score: 390

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
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- 7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	7	US-10-103-686-1
c 2	327.6	84.0	1640	6	Sequence 1, Appli
c 3	326.6	83.7	1597	6	Sequence 13206, A
4	324.4	83.2	408	5	Sequence 13540, A
5	324.4	83.2	421	5	Sequence 36573, A
6	313.2	80.3	1597	6	Sequence 16692, A
7	311.6	79.9	420	5	Sequence 13540, A
8	305.4	78.3	1636	5	Sequence 16500, A
9	305.4	78.3	1636	5	Sequence 22578, A
10	301.8	77.4	883	7	Sequence 28418, A
c 11	300.6	77.1	2667	7	Sequence 73, Appl
12	295.2	75.7	548	6	Sequence 267, Appl
c 13	295.2	75.7	1636	5	Sequence 76, Appl
c 14	295.2	75.7	1636	5	Sequence 22578, A
15	288	73.8	413	5	Sequence 28418, A
16	285.4	73.2	735	7	Sequence 16199, A
17	285.4	73.2	735	7	Sequence 59, Appl
18	285.4	73.2	735	7	Sequence 63, Appl
19	285.4	73.2	735	7	Sequence 64, Appl
20	285.4	73.2	735	7	Sequence 59, Appl
21	285.4	73.2	735	7	Sequence 63, Appl
22	284.6	73.0	331	1	Sequence 64, Appl
23	284.6	73.0	331	1	Sequence 200, App
24	284.4	72.9	726	1	Sequence 200, App
25	284.4	72.9	726	7	Sequence 4, Appli

26	281.2	72.1	747	5	US-09-959-373A-1	Sequence 1, Appli
27	281.2	72.1	819	1	PCT-US02-18947-198	Sequence 198, App
28	281.2	72.1	819	7	US-10-172-118-198	Sequence 198, App
c 29	280.4	71.9	12220	5	US-09-919-002-67	Sequence 67, Appl
30	279.6	71.7	435	5	US-09-918-995-16554	Sequence 16554, A
31	275.8	70.7	735	7	US-10-039-785-54	Sequence 54, Appl
32	275.8	70.7	735	7	US-10-139-785-54	Sequence 54, Appl
c 33	275.8	70.7	735	7	US-10-139-785-54	Sequence 54, Appl
34	273.2	70.5	707	7	US-10-027-632-18093	Sequence 18093, A
35	269.4	69.1	530	5	US-09-785-276A-56598	Sequence 56598, A
36	269.4	69.1	735	7	US-10-039-785-57	Sequence 57, Appl
37	267.8	68.7	735	7	US-10-139-785-57	Sequence 57, Appl
38	267.8	68.7	735	7	US-10-039-785-60	Sequence 60, Appl
39	261.4	67.0	735	7	US-10-139-785-60	Sequence 60, Appl
40	261.4	67.0	735	7	US-10-039-785-58	Sequence 58, Appl
41	261.4	67.0	735	7	US-10-039-785-61	Sequence 61, Appl
42	261.4	67.0	735	7	US-10-139-785-61	Sequence 61, Appl
43	258.2	66.2	735	7	US-10-039-785-55	Sequence 55, Appl
44	258.2	66.2	735	7	US-10-139-785-55	Sequence 55, Appl
45	237.6	66.1	496	5	US-09-918-995-37811	Sequence 37811, A

#### ALIGNMENTS

#### RESULT 1

US-10-103-686-1

; Sequence 1, Application US/10103686

; GENERAL INFORMATION:

; APPLICANT: REFF, Mitchell E.

; KLOETZER, William S.

; NAKAMURA, Takehiko

; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/103,686

; FILING DATE: 25-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/803,085

; FILING DATE: 20-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 390 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..390

; FEATURE:

; NAME/KEY: mat\_peptide

```
; LOCATION: 58..390
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

Query Match      100.0%; Score 390; DB 7; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCTGACTCTGCTCTGCTACCCCTCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
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Db 1 ATGGCGCTGACTCTGCTCTGCTACCCCTCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
    |||||
Qy 61 TCTGCCCGGACTCAGCCCTCTCTGTCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||
Db 61 TCTGCCCGGACTCAGCCCTCTCTGTCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||
Qy 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATATGCTCTCGTGTACCAACACCAC 180
    |||||
Db 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATATGCTCTCGTGTACCAACACCAC 180
    |||||
Qy 181 CCAGGCAAGCCGCCAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTCTCT 240
    |||||
Db 181 CCAGGCAAGCCGCCAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTCTCT 240
    |||||
Qy 241 GATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||
Db 241 GATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||
Qy 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACCAACAGTAGACACTTTGTTATTTC 360
    |||||
Db 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACCAACAGTAGACACTTTGTTATTTC 360
    |||||
Qy 361 GGAAGAGGACCGGCTTGACCGTCTCTAGGT 390
    |||||
Db 361 GGAAGAGGACCGGCTTGACCGTCTCTAGGT 390

RESULT 2
US-10-198-846-13206/c
; Sequence 13206, Application US/10198846
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13206
; LENGTH: 1640
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13206

Query Match      84.0%; Score 327.6; DB 6; Length 1640;
Best Local Similarity 90.0%; Pred. No. 2.3e-80;
Matches 351; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 ATGGCGCTGACTCTGCTCTGCTACCCCTCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
    |||||
Db 1569 ATGGCGCTGGGCTCTGCTCTCTCAGCCTCTCTCACTCAGGCGACAGGATCCTGGGCTCAG 1510
    |||||
Qy 61 TCTGCCCGGACTCAGCCCTCTGTCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||

; LOCATION: 58..390
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-103-686-1

Query Match      100.0%; Score 390; DB 7; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.2e-97;
Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCTGACTCTGCTCTGCTACCCCTCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
    |||||
Db 1 ATGGCGCTGACTCTGCTCTGCTACCCCTCTCACTCAGGCGACAGGATCCTGGGCTCAG 60
    |||||
Qy 61 TCTGCCCGGACTCAGCCCTCTCTGTCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||
Db 61 TCTGCCCGGACTCAGCCCTCTCTGTCTGGGTCTCTCGACACGTCGGTCACCATCTCC 120
    |||||
Qy 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATATGCTCTCGTGTACCAACACCAC 180
    |||||
Db 121 TGCACCTGGACACGAGGATGACGTTGGTGGTTATATGCTCTCGTGTACCAACACCAC 180
    |||||
Qy 181 CCAGGCAAGCCGCCAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTCTCT 240
    |||||
Db 181 CCAGGCAAGCCGCCAACTCATGATTTATGATGTCGTAAGCGGCGCTCAGGGGTCTCT 240
    |||||
Qy 241 GATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||
Db 241 GATCGCTTCTCTGGTCTCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG 300
    |||||
Qy 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACCAACAGTAGACACTTTGTTATTTC 360
    |||||
Db 301 GCTGAGGACGAGGCTGATTTACTGTTGTCATATACCAACAGTAGACACTTTGTTATTTC 360
    |||||
Qy 361 GGAAGAGGACCGGCTTGACCGTCTCTAGGT 390
    |||||
Db 361 GGAAGAGGACCGGCTTGACCGTCTCTAGGT 390

RESULT 3
US-10-198-846-13540/c
; Sequence 13540, Application US/10198846
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13540
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-13540

Query Match      83.7%; Score 326.5; DB 6; Length 1597;
Best Local Similarity 90.0%; Pred. No. 4.3e-80;
Matches 350; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 2 TGGCGCTGGACTCTGCTCTGCTCCTCGCTCACCCCTCTCACTCAGGCGACAGGATCCTGGGCTCAGT 61
    |||||
Db 1529 TGGCGCTGGGCTCTGCTCTGCTCCTCGCTCACCCCTCTCACTCAGGCGACAGGCTCTGGGCCCCAGT 1470
    |||||
Qy 62 CTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCTCGGACAGTCGGTCACCATCTCTCT 121
    |||||
Db 1469 CTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCTCGGACAGTCGATCACCATCTCTCT 1410
    |||||
Qy 122 GCACCTGGAAACGAGGATGACGTTGGTGGTTATATGCTCTCTCGGTACCAACACCACC 181
    |||||
Db 1409 GCATTGGAAACCTCAATGACATTTGTTAGTTATTAATATGTTCTTCTGTTTCCAACACCACC 1350
    |||||
Qy 182 CAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGGGGCGCTCAGGGGTCTCTG 241
    |||||
Db 1349 CAGGCAAGCCCCCAAACTCATGATTTATGATGTCAGTAATCGGGCGCTCAGGGGTTCTTA 1290
    |||||
Qy 242 ATCGCTTCTCTGGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGG 301
    |||||
Db 1289 ATCGCTTCTCTGGGTCCCAAGTCTGGCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAGG 1230
    |||||
Qy 302 CTGAGGACGAGGCTGATTTACTGTTGTTATATACCAACAGTAGACACTTTGTTATTTCG 361
    |||||
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Query Match	79.9%;	Score 311.6;	DB 5;	Length 420;
Best Local Similarity	87.4%;	Pred. No. 4..6e-76;		
Matches 341;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps
QY 1	ATGGCCTGGACTCTGCTCTCTGCTCAGCTCCTCACTCAGGGCACAGGATCTCTGGGCTCAG	60		
Db 25	atggcctgggctgtattctctcaacctctctcactcagggcacagggtctctgggccag	84		
QY 61	TC TGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTTGAGACGTGCTCACCATCTCC	120		
Db 85	tc tggcctgactcagcctgctctcg tgtctgggtctcttggctcagtcgataccactctcc	144		
QY 121	TGCAC TGGAA CCGCATGACGCTTGGTGTATTAACATATGCTCTGCTGTTACCAACACCAC	180		
Db 145	tgcacttggaaaccagatgcattgggtgcttctaactatgtctctctgtaccacaccac	204		
QY 181	CCAGGCAAGCCCCCAACTCATGATTTATGATGTGCTTAAGCGGGCTCTCAGGGGTCTCT	240		
Db 205	cgggcaaaagcccccaactcattattataatgcagtgcgcccctcagggtttct	264		
QY 241	GATCGCTTCTCTGGCTCCAAAGCTGGCAACAGGCCTCCCTGACCATCTCTGGGCTCCAG	300		
Db 265	aatcgctctctggctccaagtctggcaacacggcctcctcaacgctctcgggtccag	324		







```
OY 191 CCCCCAACTCATGATTTATGATGTCGTAAAGCGGCGCTCAGGGGTCTCTGATCGCTTCT 250
|||||
Db 1372 CCCCCAACTCTGATTTATGAGTCAAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCT 1313
|||||
OY 251 CTGGCTCCAAGTCTGGACACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 310
|||||
Db 1312 CTGGCTCCAAGTCTGGACACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 1253
|||||
OY 311 AGGCTGATTATTACTGTTGTTTCATATACACAGCAGTAGCATTGTTA-----TTCGGAA 364
|||||
Db 1252 AGGCTGATTATTACTGACCTTCATACACAGCAGCAGCAGTGTGTGTTGTTCTTCGGAA 1193
|||||
OY 365 GAGGACCGGTTGACCGTCTAGGT 390
|||||
Db 1192 CTGGGACCAAGGTCACCGTCTAGGT 1167
|||||

RESULT 14
US-09-785-276A-28418/c
; Sequence 28418, Application US/09785276A
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007B
; CURRENT APPLICATION NUMBER: US/09/785,276A
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28418
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-785-276A-28418

Query Match 75.7%; Score 295.2; DB 5; Length 1636;
Best Local Similarity 87.3%; Pred. No. 1.9e-71;
Matches 337; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

OY 11 CTCGTCTCTGTGACCCCTCCTCACTCAGGCGACAGGATCTCTGGGCTCAGTGTGCCCGCA 70
|||||
Db 1552 CACTCTCTCTCTCACCCTCCTCACTCAGGACACAGGGTCTCTGGGCCAGTCTGCCCTGA 1493
|||||
OY 71 CTCAGCTCCCTCTGTCTGGGTCTCTCTGGACAGTCTCGGTCAACCATCTCTGCACCTGGAA 130
|||||
Db 1492 CTCACCTGCCCGGTCTGGGTCTCTCTGGACAGTCTCGGTCAACCATCTCTGCACCTGGAA 1433
|||||
OY 131 CCAGCGATGACGTGTGGTGTATTAACATATGTCCTGGTACCAACACACCCAGGCAAG 190
|||||
Db 1432 CCAGCGATGCTGTGGATTTATTAATCTTCTCTGGTACCAACAGCAGCAGGCAAG 1373
|||||
OY 191 CCCCCAACTCATGATTTATGATGTCGTAAAGCGGCGCTCAGGGGTCTCTGATCGCTTCT 250
|||||
Db 1372 CCCCCAACTCTGATTTATGAGTCAAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCT 1313
|||||
OY 251 CTGGCTCCAAGTCTGGACACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 310
|||||
```

```
Db 1312 CTGGCTCCAAGTCTGGACACAGCGGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 1253
|||||
OY 311 AGGCTGATTATTACTGTTGTTTCATATACACAGCAGTAGCATTGTTA-----TTCGGAA 364
|||||
Db 1252 AGGCTGATTATTACTGACCTTCATACACAGCAGCAGCAGTGTGTGTTGTTCTTCGGAA 1193
|||||
OY 365 GAGGACCGGTTGACCGTCTAGGT 390
|||||
Db 1192 CTGGGACCAAGGTCACCGTCTAGGT 1167
|||||

RESULT 15
US-09-918-995-16199
; Sequence 16199, Application US/09918995
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16199
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(413)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-16199

Query Match 73.8%; Score 288; DB 5; Length 413;
Best Local Similarity 84.4%; Pred. No. 1.4e-69;
Matches 324; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

OY 1 ATGGCTGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
|||||
Db 29 atggctgggtctctctctctctctctctctctctctctctctctctctctctctctctct 88
|||||
OY 61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCTGGACAGTCGGTCAACCATCTCC 120
|||||
Db 89 tctgcctgaactcagcctgcctcctgtctgtgtctcctggagcagtcgatcaccatctcc 148
|||||
OY 121 TGCACCTGGAAACGACGATGACGCTGTGGTGTATTAACATATGTCCTGTGTACCAACACAC 180
|||||
Db 149 tgcactgggaatcagcagtgacgtggtgattataggagtgtctcctctggcaccactgcac 208
|||||
OY 181 CCAGGCAAGCCCCCAACTCATGATTTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCT 240
|||||
Db 209 ccaggcaagcccccaagtcataattatgatgcaataatttcggccctcaggggttct 268
|||||
OY 241 GATCGCTTCTCTGGCTCCAAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||
Db 269 aatcgcttctcgtcccaagtctggcaacacggtcctcctctgagcatctctgggtccag 328
|||||
OY 301 GCTGAGGACGAGGTGATTTATTACTGTTTTCATATACACAGTACGACTTTGTTATTTC 360
|||||
Db 329 gctgaggacaggtgtaattactgagctcatatacaaacaccacaccccccttat 388
|||||
OY 361 GGAAGAGGACCGGTTGACCGTC 384
|||||
Db 389 gctctcgggaactgggaccaaggtc 412
|||||
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Search completed: September 23, 2002, 19:58:38  
Job time: 7168 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:07:09 ; Search time 110.65 Seconds  
(without alignments)  
865.767 Million cell updates/sec

Title: US-09-019-441-1  
Perfect score: 390  
Sequence: 1 ATGGCTGACTCTGCTCCT.....CCGGTTGACGCTCCTAGGT 390

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match %	Length DB ID	Description	
1	390	100.0	390	US-08-803-085-1	Sequence 1, Appli
2	321.2	82.4	891	US-09-049-672A-23	Sequence 23, Appl
3	319.6	81.9	902	US-08-378-939-11	Sequence 11, Appl
4	275.4	70.6	333	US-08-958-201-13	Sequence 13, Appl
5	273.8	70.2	333	US-08-958-201-11	Sequence 11, Appl
6	239.6	61.4	324	US-09-240-274-137	Sequence 137, App
7	234.6	60.2	935	US-09-049-672A-20	Sequence 20, Appl
8	233	59.7	771	US-08-305-683A-3	Sequence 3, Appli
9	225.8	57.9	393	US-08-991-789A-241	Sequence 241, App
10	225.8	57.9	771	US-09-062-451-241	Sequence 241, App
11	208.8	53.5	312	US-09-240-274-138	Sequence 138, App
12	194.8	49.9	396	US-08-345-321-3	Sequence 3, Appli
13	194.6	49.9	711	US-08-487-550-9	Sequence 9, Appli
14	194.6	49.9	895	US-09-049-672A-25	Sequence 25, Appl
15	192.8	49.4	933	US-09-079-029-8	Sequence 8, Appli
16	192	49.2	333	US-08-652-816A-27	Sequence 27, Appl
17	183.2	47.0	774	US-08-665-202-4	Sequence 4, Appli
18	179	45.9	336	US-09-240-274-133	Sequence 133, App
19	178.6	45.8	330	US-09-240-274-132	Sequence 132, App
20	176.2	45.2	330	US-08-199-911-1	Sequence 1, Appli
21	172.8	44.3	333	US-08-477-553A-43	Sequence 43, Appl
22	169	43.3	330	US-09-240-274-134	Sequence 134, App
23	168	43.1	333	US-08-264-093-5	Sequence 5, Appli
24	167.2	42.9	908	US-09-273-839A-9	Sequence 9, Appli
25	164.2	42.1	327	US-09-240-274-126	Sequence 126, App
26	164.2	42.1	327	US-09-240-274-223	Sequence 223, App
27	164.2	42.1	450	US-08-966-316-5	Sequence 5, Appli

28	162.6	41.7	327	4	US-09-240-274-129	Sequence 129, App
29	161	41.3	327	4	US-09-240-274-128	Sequence 128, App
30	161	41.3	327	4	US-09-240-274-130	Sequence 130, App
31	158.8	40.7	431	2	US-08-345-321-7	Sequence 7, Appli
32	158.2	40.6	342	4	US-09-240-274-131	Sequence 131, App
33	153.6	39.4	327	4	US-09-240-274-124	Sequence 124, App
34	153.2	39.3	919	3	US-09-049-672A-24	Sequence 24, Appl
35	153	39.2	327	4	US-09-240-274-123	Sequence 123, App
36	153	39.2	327	4	US-09-240-274-125	Sequence 125, App
37	150.6	38.6	705	3	US-08-487-550-1	Sequence 1, Appli
38	149	38.2	387	1	US-08-379-072A-20	Sequence 20, Appl
39	149	38.2	387	1	US-08-478-039-109	Sequence 109, App
40	149	38.2	387	1	US-08-481-869-20	Sequence 20, Appl
41	149	38.2	387	1	US-08-476-349A-109	Sequence 109, App
42	149	38.2	387	1	US-08-476-237-16	Sequence 16, Appl
43	149	38.2	387	3	US-08-523-894-3	Sequence 3, Appli
44	149	38.2	702	3	US-08-523-894-5	Sequence 5, Appli
45	147	37.7	312	2	US-08-273-146-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1  
US-08-803-085-1  
; Sequence 1, Application US/08803085  
; Patent No. 6011138  
; GENERAL INFORMATION:  
; APPLICANT: REFF, Mitchell E.  
; APPLICANT: KLOETZER, William S.  
; APPLICANT: NAKAMURA, Takehiko  
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P. O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/803,085  
; FILING DATE: 20-FEB-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-353  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 390 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..390  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 58..390  
US-08-803-085-1

Query Match	100.0%;	Score 390;	DB 3;	Length 390;
Best Local Similarity	100.0%;	Pred. No. 3.3e-106;		
Matches 390;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGSCCTGGACTCTGCTCCGTCACCCCTCCTCAGTACAGGCACAGATCTCTGGGCTCAG	60	
Db	1	ATGSCCTGGACTCTGCTCCGTCACCCCTCCTCAGTACAGGCACAGATCTCTGGGCTCAG	60	
QY	61	TCTGCCCCGACTCAGCCTCCCTCTGTGCTCTGGGTCTCCTGGACAGTCGGTACCACTTC	120	
Db	61	TCTGCCCCGACTCAGCCTCCCTCTGTGCTCTGGGTCTCCTGGACAGTCGGTACCACTTC	120	
QY	121	TGCACTGGAAACCGATGACGTTGGTGGTTAATACTATGTCTCTGGGTACCAACACCAC	180	
Db	121	TGCACTGGAAACCGATGACGTTGGTGGTTAATACTATGTCTCTGGGTACCAACACCAC	180	
QY	181	CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT	240	
Db	181	CCAGGCAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT	240	
QY	241	GATCGCTTCTCTGGCTCCAAGTCTGGCAACAGGCGCTCCCTGACCATCTCTCTGGGCTCCAG	300	
Db	241	GATCGCTTCTCTGGCTCCAAGTCTGGCAACAGGCGCTCCCTGACCATCTCTCTGGGCTCCAG	300	
QY	301	GCTGAGGACGAGGCTGATTTATTACTGTGTTATATACACAGTAGTACGACTTGTATTTC	360	
Db	301	GCTGAGGACGAGGCTGATTTATTACTGTGTTATATACACAGTAGTACGACTTGTATTTC	360	
QY	361	GGAAGAGGGACCCGGTTGACCGTCTCTAGGT	390	
Db	361	GGAAGAGGGACCCGGTTGACCGTCTCTAGGT	390	

## RESULT 2

```

US-09-049-672A-23
;
; Sequence 23, Application US/09049672A
; Patent No. 6135941
;
; GENERAL INFORMATION:
;
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
;
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
;
; NUMBER OF SEQUENCES: 28
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```

34304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows  
 CURRENT APPLICATION DATA: Version 2.0  
 APPLICATION NUMBER: US/09/049,672A  
 FILING DATE: HEREWITH  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cerrone, Michael C  
 REGISTRATION NUMBER: 39,132  
 REFERENCE/DOCKET NUMBER: PF-0497 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 891 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: THYRN0T10  
CLONE: 2872705  
US-09-049-672A-23

Query Match	82.4%;	Score 321.2;	DB 3;	Length 891;
Best Local Similarity	89.0%;	Pred. No. 8.5e-86;		
Matches 347;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps
QY 1	ATGSCCTGGACTCTGCNCTCGCTCACCCCTCCTCACTCAGGGCACAGGATCTCTGGGCTCAG	60		
Db 34	ATGSCCTGGGCTCTGCTATTCTCTCACCCCTCCTCACTCAGGGCACAGGCTCTGGGCGCAG	93		
QY 61	TCTGCCCGGACTCAGGCTCCCTCTGTGTCCTGGGTCCTCTGGACAGTCGGTGACCACTCTCC	120		
Db 94	TCTGCCCTGACTCAGGCTCGCTCCGTCTGTCGGTCTCCTGGACAGTCGATCACCATCTCC	153		
QY 121	TGCACGTGAACACCGGATGACGTTGGTGGTTATTAACATATGTCCTCGGTACCAACACCAC	180		
Db 154	TGCACGTGAACACGACGATGACGTTGGTGGTTATTAACATATGTCCTCGGTACCAACACGTC	213		
QY 181	CCAGGCAAGGCCCCCAAACTCATGATTTATGATGTCGCCTAAGGGGCCCTCAGGGGTCTCT	240		
Db 214	CCAGGCACGGCCCCCAAACTCATGATTTATGAGGTCAGTAACTCGGCCCTCAGGGGTCTCT	273		
QY 241	GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCCTCCCTGACCAATCTCTGGGCTCCAG	300		
Db 274	AATCGGTTCTCTGGCTCCAAGTCTGGCAACACGGCCCTCCCTGACCAATCTCTGGGCTCCAG	333		
QY 301	GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACACCAAGTAGCACTTTGTATTATTC	360		
Db 334	GCTGAGGACGAGGCTGATTATTACTGCTATATAGGCAACCAATTTGTGGTATTTC	393		
QY 361	GGAAAGGAGCACCGGTTGACCGTCCTAGGT	390		
Db 394	GGCGGAGGAGCAACAGCTGACCGCTCTAGGT	423		

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RESULT      3
US-08-378-939-11
; Sequence 11, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTIETH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```



;/ TITLE OF INVENTION: materials and methods  
;/ NUMBER OF SEQUENCES: 23  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
;/ STREET: 6300 Sears Tower, 233 South Wacker Drive  
;/ CITY: Chicago  
;/ STATE: Illinois  
;/ COUNTRY: USA  
;/ ZIP: 60606-6402  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/958,201  
;/ FILING DATE:  
;/ PRIORITY APPLICATION DATA:  
;/ APPLICATION NUMBER: US 60/028,897  
;/ FILING DATE: 21-OCT-1996  
;/ INFORMATION FOR SEQ ID NO: 11:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 333 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: double  
;/ TOPOLOGY: linear  
;/ IMMEDIATE SOURCE:  
;/ CLONE: D12 (light chain)  
;/ FEATURE:  
;/ NAME/KEY: CDS  
;/ LOCATION: 1..333  
;/ US-08-958-201-11

Query Match 70.2%; Score 273.8; DB 2; Length 333;  
Best Local Similarity 88.9%; Pred. No. 6e-72; Indels 0; Gaps 0;  
Matches 236; Conservative 0; Mismatches 37;  
QY 58 CAGTCTGCCCGGACTCAGCCTCCCTCTGTCTGTGGGTCTCTCTGGACAGTCGGTCAACATC 117  
Db 1 CAGTCTGCTGACTCAGCCTGCCTCTGTCTGTGGGTCTCTCTGGACAGTCGATCACCATC 60  
QY 118 TCCTGCACTGGACAGCAGTACGTGGTGGTTTATACTATGTCTCTGGTACCAACAC 177  
Db 61 TCCTGCACTGGACAGCAGTACGTGGTGGTTTATACTATGTCTCTGGTACCAACAC 120  
QY 178 CACCCAGGCAAAACCCCAACATCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 237  
Db 121 CACCCAGGCAAAACCCCAACATCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTC 180  
QY 238 TCTGATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGCGCCCTCCCTGACCATCTCTGGGCTC 297  
Db 181 CCTAATCGCTTCTCAGGCTCCAAAGTCTGGCAACACAGCGCCCTCCCTGACCATCTCTGGGCTC 240  
QY 298 CAGGCTGAGCAGCAGCTGATTATTACTGTTTATATATACACAGTAGCAGCTTTGTTA 357  
Db 241 CAGGTTGAGCAGCAGCTGATTATTACTGAGCTCACTTACACGACAGTCACTGTGATC 300  
QY 358 TTCCGAAGAGGAGGACCGGTTGACCGTCCTAGGT 390  
Db 301 TTCCGGGAGGAGGACCAAGCTGACCGTCTAGGT 333

RESULT 6  
US-09-240-274-137  
; Sequence 137, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/240,274

;/ CURRENT FILING DATE: 1999-01-29  
;/ EARLIER APPLICATION NUMBER: 60/081,380  
;/ EARLIER FILING DATE: 1998-04-10  
;/ EARLIER APPLICATION NUMBER: 60/028,550  
;/ EARLIER FILING DATE: 1996-10-11  
;/ NUMBER OF SEQ ID NOS: 224  
;/ SOFTWARE: PatentIn Ver. 2.0  
;/ SEQ ID NO 137  
;/ LENGTH: 324  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
;/ FEATURE:  
;/ OTHER INFORMATION: anti-Rh(D) chain R01  
;/ US-09-240-274-137

Query Match 61.4%; Score 239.6; DB 4; Length 324;  
Best Local Similarity 86.8%; Pred. No. 7.4e-62;  
Matches 276; Conservative 0; Mismatches 39; Indels 3; Gaps 1;  
QY 70 ACTCAGCCTCCCTCTCTGTCTGTGGTCTCTCTGGACAGTCGGTCAACATCTCTCTGCCTGGA 129  
Db 10 actcagctccctcccgctccgggtctctggacagtcagtcacctctctctgactgga 69  
QY 130 ACCAGCGATGACGTTGGTGGTTATAACTATGTCTCTGTGTACCAACACACCCAGGCAAA 189  
Db 70 gccagcagtgagtggtgtcttataagcagctctctctgtgtaccaacaacacccagcaaa 129  
QY 190 GCCCCCAAACTCATGATTATGATGTCGCTAAGCGGGCTCAGGGGTCTCTGTATCCTTC 249  
Db 130 gcccccacactctgactcatgagggcactaaagcgcctcaggggtccctgactccttc 189  
QY 250 TCTGGCTCCAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGCTCCAGGCTGAGGAC 309  
Db 190 tctggctccaagctctggcaacacgctccctgacagctctctggctccaggtgaggt 249  
QY 310 GAGGCTGATTATTACTGTTGTTTCATATACACAGTAGCAGCTTTGTTATTCGGAAGAGG 369  
Db 250 gaggtgattattactgcagctcatttga---ggLaattccgtgatatttcggcgagg 306  
QY 370 ACCCGGTTGACGTCCTCA 387  
Db 307 accaagctgaccgtccta 324

RESULT 7  
US-09-049-672A-20  
; Sequence 20, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:





US-08-991-789A-241/c  
; Sequence 241, Application US/08991789A  
; Patent No. 6225054  
; GENERAL INFORMATION:  
; APPLICANT: Fridakis, Tony N.  
; Smith, John M.  
; Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 292  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed IP Law Group  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/991,789A  
; FILING DATE: 11-Dec-1997  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 210121.419C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 241:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 771 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; SEQUENCE DESCRIPTION: SEQ ID NO: 241:  
US-08-991-789A-241

Query Match 57.9%; Score 225.8; DB 4; Length 771;  
Best Local Similarity 89.0%; Pred. No. 1.1e-57;  
Matches 242; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 119 CCTGCACTGGAACACGACGATGAGTGGTGGTTATTAACATATGTCCTCGGTACCAACACC 178  
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Db 448 CCTGCANTGGAACACGACGATGAGTGGTGGTTATTAATAATGTCCTCGGTACCAACACC 389  
QY 179 ACCGAGGAAAGCCCAACATCATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTCT 238  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 388 ACCAGGCAAGCCCAACATCATGATTATGAGTGGTGAATCGGCCCTCAGGGGTCT 329  
QY 239 CTGATCGCTTCTCTGCTCCAAAGTCGCAACACGCGCTCCCTGACCATCTCTGGGCTCC 298  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 328 CTAATCGCTTCTCTGCTCCAAAGTCGCAACACGCGCTCCCTGACCATCTCTGGGCTCC 269  
QY 299 AGGCTGAGGACGAGGCTGATTATTAATGTTTCATATACAACACGATAGCACTTTGTTAT 358  
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Db 268 AGGCTGAGGACGAGGCTGATTATTAATGTCAGCTCATATACAAGCAGCAGCACTCTCGTGT 209  
QY 359 TCGGAAGAGGGACCGGGTTGACCGTCTAGGT 390  
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Db 208 TTGGCGGAGGGACCAAGCTGACCGTCTAGGT 177

RESULT 10  
US-09-062-451-241/c

; Sequence 241, Application US/09062451  
; Patent No. 6344550  
; GENERAL INFORMATION:  
; APPLICANT: Fridakis, Tony N.  
; Smith, John M.  
; Reed, Steven G.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 297  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/062,451  
; FILING DATE: 04-APR-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.419C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 241:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 771 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-09-062-451-241  
Query Match 57.9%; Score 225.8; DB 4; Length 771;  
Best Local Similarity 89.0%; Pred. No. 1.1e-57;  
Matches 242; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 119 CCTGCACTGGAACACGACGATGAGTGGTGGTTATTAACATATGTCCTCGGTACCAACACC 178  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 448 CCTGCANTGGAACACGACGATGAGTGGTGGTTATTAATAATGTCCTCGGTACCAACACC 389  
QY 179 ACCGAGGAAAGCCCAACATCATGATTATGATGTCGCTAAGCGGGCCTCAGGGGTCT 238  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 388 ACCAGGCAAGCCCAACATCATGATTATGAGTGGTGAATCGGCCCTCAGGGGTCT 329  
QY 239 CTGATCGCTTCTCTGCTCCAAAGTCGCAACACGCGCTCCCTGACCATCTCTGGGCTCC 298  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 328 CTAATCGCTTCTCTGCTCCAAAGTCGCAACACGCGCTCCCTGACCATCTCTGGGCTCC 269  
QY 299 AGGCTGAGGACGAGGCTGATTATTAATGTTTCATATACAACACGATAGCACTTTGTTAT 358  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 268 AGGCTGAGGACGAGGCTGATTATTAATGTCAGCTCATATACAAGCAGCAGCACTCTCGTGT 209  
QY 359 TCGGAAGAGGGACCGGGTTGACCGTCTAGGT 390  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Db 208 TTGGCGGAGGGACCAAGCTGACCGTCTAGGT 177

RESULT 11  
US-09-240-274-138  
; Sequence 138, Application US/09240274  
; Patent No. 6255455



```

, ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
, STREET: 699 Prince Street
, CITY: Alexandria
, STATE: VA
, COUNTRY: USA
, ZIP: 22314
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.30
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/487,550
, FILING DATE: 07-JUN-1995
, CLASSIFICATION: 435
, ATTORNEY/AGENT INFORMATION:
, NAME: Teskin, Robin L.
, REGISTRATION NUMBER: 35,030
, REFERENCE/DOCKET NUMBER: 012712-131
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 703-836-6620
, TELEFAX: 703-836-2021
, INFORMATION FOR SEQ ID NO: 9:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 711 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: not relevant
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
, FEATURE:
, NAME/KEY: CDS
, LOCATION: 1..711
, FEATURE:
, NAME/KEY: mat_peptide
, LOCATION: 1..711
, PS-08-487-550-9

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Query Match 49.9%; Score 194.6; DB 3; Length 711;  
Best Local Similarity 72.0%; Pred. No. 1.8e-48;  
Matches 283; Conservative 0; Mismatches 104; Indels 6; Gaps 2;

Qy	1	ATGGCCTGGAGACTGCTGCTCTGTCGACACCCCTCTCTCATTACAGGGCACAGGATCTCTGGGCTCAG	60
Db	4	AGGGTCCCCGCTCAGCTCTGAGCTGGGGTCTCTGCTCTGCTGCCAGTGCACGATGTGAG	63
Qy	61	TC TGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCCCTGGACAGTCGGTCACCATCTCC	120
Db	64	TC TGCTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAAGTCAACCATCTCG	123
Qy	121	TGCACCTGGAAACGCGATGACGTTGGTGGTTATTAACATGTCTCTGGTACCAACACCCAC	180
Db	124	TGCACCTGGGAGCACCCTCCAAACATTGGAGGTTAT--GATCTACATGGTACCAAGAGCTC	180
Qy	181	CCAGGCAAGAGCCCCCAAACTCATGATTTATGATGTGGCTTAAGGGGCCCTCAGGGGTCTCT	240
Db	181	CCAGGAACGGCCCCCAAACTCTCATCTATGACATTTAACAACGACCCCTCAGGAATTTCT	240
Qy	241	GATCGGCTTCTCTGGCTCCAGTCTGCCAACAGCGGCTCCCTGACCATCTCTGGGCTCCAG	300
Db	241	GACCGAATCTCTGGCTCCAAGTCTGGTACGGGGGCTCCCTGGCCATCACTGGGCTCCAG	300
Qy	301	GCTGAGGACGAGGCTGATTATTACTGTTTTCATATACAAACCAG--TAGCATCTTTGTTA	357
Db	301	ACTGAGGATGAGGCTGATTATTACTTCCAGTCTCTATGACAGCAGCCTGAATCTCAGGTA	360
Qy	358	TTCCGGAAGAGGGACCCGGTTGACCGTCTTAGGT	390
Db	361	TTCCGGAAGAGGGACCCGGCTGACCGTCTTAGGT	393

RESULT • 14

US-09-049-672A-25

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> Sequence 25, Application US/09049672A
> Patent No. 6135941
> GENERAL INFORMATION:
> APPLICANT: Hillman, Jennifer L.
> APPLICANT: Lal, Preeti
> APPLICANT: Tang, Y. Tom
> APPLICANT: Yue, Henry
> APPLICANT: Au-Young, Janice
> APPLICANT: Corley, Neil C.
> APPLICANT: Guegler, Karl J.
> APPLICANT: Baughn, Mariah R.
> TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
> NUMBER OF SEQUENCES: 28
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: Incyte Pharmaceuticals, Inc.
> STREET: 3174 Porter Drive
> CITY: Palo Alto
> STATE: CA
> COUNTRY: USA
> ZIP: 94304
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Diskette
> COMPUTER: IBM Compatible
> OPERATING SYSTEM: DOS
> SOFTWARE: FastSeq for Windows Version 2.0
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/09/049,672A
> FILING DATE: HEREWITH
> CLASSIFICATION: 536
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER:
> FILING DATE:
> ATTORNEY/AGENT INFORMATION:
> NAME: Cerrone, Michael C.
> REGISTRATION NUMBER: 39,132
> REFERENCE/DOCKET NUMBER: PF-0497 US
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 650-855-0555
> TELEFAX: 650-845-4166
> TELEX:
> INFORMATION FOR SEQ ID NO: 25:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 895 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> IMMEDIATE SOURCE:
> LIBRARY: LUNGUT13
> CLONE: 3116314
>
> US-09-049-672A-25

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Query Match	49.94;	Score	194.6;	DB 3;	Length	895;			
Best Local Similarity	72.0%;	Pred. No.	1.9e-48;						
Matches	283;	Conservative	0;	Mismatches	104;	Indels	6;	Gaps	2;
Qy	1	ATGGCCTGGACTCTGCTCCTCGTCAACCTCTCACTCAGGGCACAGGATCCTGGGCTCAG	60						
Db	37	ATGGCGGCTTCCTCTCCTCTCGCCCTCTCACTCACTGTGCAGGGTCTCTGGGCCAC	96						
Qy	61	TCTGCCCGGATCAGCCCTCTGTGTCCTGGGTCTCTGGACATCTGGTCAACCATGCC	120						
Db	97	TCTGTGTGACTCAGCCCCCTCAGCGTCTGGGACCCCCGGCAGAGGTCACCATCTCT	156						
Qy	121	TGCATCTGAAACACGCGATGAGTGGTGGTATTAATACTATCTCTCGTGTACCAACACCCAC	180						
Db	157	TGTTCTGGAACCACTCCAACATCGCAAG---TAATTCTGTGCATTGGTACCAATTAGTT	213						
Qy	181	CCAGGCAAGAGCCCAACTCATGTTTATGATGTGCTTAAGCGGGCCCTCAGGGGTCTCT	240						
Db	214	CCAGGAGCGGGCCCCAAACTCTCATCTATGCTAATGATCAGCGTGCCTCGGGGTCCCT	273						
Qy	241	GATCGCTTCTCTGGCTCCAAAGTCTGGCAACACAGGGCCTCCCTGACCATCTCTGGGCTCCAG	300						

Db 274 GACCGATCTCTGGCTCCAAAGCTGACCTAGCCCTCCCTGGCCATCAGTGGGCTCCGG 333  
QY 301 GCTGAGGACGAGGCTGATTACTGTTGTTTCATATACAAACAGT---AGCACTTTGTTA 357  
Db 334 CCGAGGATGAACACTGATTACTCTGCAACATGGATGACAGTCTCAGTGGTTGGATG 393  
QY 358 TTCGGAAGAGGACCGCGTTGACCGTCCTAGGT 390  
Db 394 TTCGGCGGAGGACCAAGCTGACCGTCCTAGGT 426

RESULT 15

US-09-079-029-8  
; Sequence 8, Application US/09079029  
; Patent No. 6342369  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Camilia W.  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Chuntharapai, Anan  
; APPLICANT: Kim, Kyung J.  
; TITLE OF INVENTION: Apo-2 Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,029  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Marschang, Diane L.  
; REGISTRATION NUMBER: 35,600  
; REFERENCE/DOCKET NUMBER: P1101R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5416  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 933 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; US-09-079-029-8

Query Match 49.4%; Score 192.8; DB 4; Length 933;  
Best Local Similarity 74.1%; Pred. No. 6.7e-48;  
Matches 258; Conservative 0; Mismatches 87; Indels 3; Gaps 1;  
QY 46 GGATCTGGGCTCAGTCTGCCCGACTACGCTCCCTCTGTCTGGGTCTCCTGGACAG 105  
Db 505 GGTGGCGGATCGCAGTCTGTGTGACGAGCGCCCTCAGTGTCTGGGCCCCAGGACAG 564  
QY 106 TCGGTCAACATCTCTGCACTGGGAGAGCTCCAACATCGGGCAGGTCTATGATGTACAC 624  
Db 565 AGGTCACCATCTCTGCACTGGGAGAGCTCCAACATCGGGCAGGTCTATGATGTACAC 624  
QY 166 TGTACCAACACCCAGGCAAGCCCAACATCATGATTATGATGTGCTAGCGG 225  
Db 625 TGTACCAACAACTTCAGGAACAGCCCCCAAACTCCTCATCTATGATGACAGCAATCGG 684  
QY 226 GCCTCAGGGGTCTCTGATCGTCTCTGGCTGCAAGTCTGGCAACACAGCGCTCCCTGACC 285

Db 685 CCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAGGTCTGGCACTCAGCTCCCTGGGC 744  
QY 286 ATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAAACAG- 344  
Db 745 ATCACTGGGCTCCAGGCTGAAGATGAGGCTGATTATTACTGCCAGTCTTATGACAGCAGC 804  
QY 345 --TAGCACTTTGTTATTTCGGAAGAGGAGGCCCGGTTGACCGTCTCTAGGT 390  
Db 805 CTGAGGGGTTCGGTATTTCGGCGGAGGAGGACCAAGGTCACCTGCTCTAGGT 852

Search completed: September 23, 2002, 18:00:46  
Job time: 3217 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:50:03 ; Search time 2581.68 Seconds  
(without alignments)  
3428.746 Million cell updates/sec

Title: US-09-019-441-2  
Perfect score: 423  
Sequence: 1 ATGAACACCTGTGGTTCTT.....TCTGTGTCACCGTCTCTCTCA 423

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg\_inv.\*  
32: em.htg\_other.\*  
33: em.htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
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1	323.8	76.5	420	9	MMU57560
2	319	75.4	420	9	MMU57565
3	318.2	75.2	411	9	MMU57563
4	315.6	74.6	423	9	HSIGHXX28
5	314.6	74.4	414	9	MMU57568
6	313.2	74.0	1431	6	AR108867
7	312.4	73.9	426	9	AF062120
8	311	73.5	420	9	HSIGHXX25
9	310	73.3	420	9	HUMIGHZF
10	309.8	73.2	468	9	HUMIGHZF
11	305.6	72.2	414	9	HSIGHXX26
12	305	72.1	414	9	HSIGHXX23
13	303.4	71.7	435	9	MMU57566
14	302.8	71.6	423	9	AF174036
15	301.8	71.3	432	9	HSIGHXX26
16	301.2	71.2	423	9	HSIGHXX20
17	299.8	70.9	1404	6	AR135375
18	299.8	70.9	1404	6	AR135376
19	299.8	70.9	1404	6	AR135377
20	299.6	70.8	423	9	AF062258
21	298.6	70.6	423	9	HST14X12
22	298.2	70.5	423	6	AR008995
23	298.2	70.5	423	6	I61194
24	298.2	70.5	423	6	I78743
25	298.2	70.5	453	9	HSE5444
26	298.2	70.5	2149	9	BC011857
27	297	70.2	423	9	HST14X24
28	296.6	70.1	429	9	AF062232
29	295.2	69.8	420	6	AR006813
30	295.2	69.8	420	6	AR135372
31	295.2	69.8	420	6	I71325
32	295	69.7	420	9	AF062220
33	294.8	69.7	423	9	HSIGHXX29
34	294.8	69.7	426	9	AF062278
35	294.6	69.6	416	9	HSIGHXX27
36	292.4	69.1	1431	6	AR108863
37	292.2	69.1	450	9	HSE55A1
38	291.8	69.0	417	9	AF062126
39	291.8	69.0	420	9	AF062101
40	291.8	69.0	420	9	AF062196
41	290.2	68.6	426	9	AF062129
42	290.2	68.6	426	9	AF062207
43	290	68.6	423	9	HSIGHXX24
44	290	68.6	456	9	HSIGH239
45	289.6	68.5	1567	6	AR135359

## ALIGNMENTS

RESULT	1
MMU57560	
LOCUS	420 bp mRNA linear PRI 11-FEB-1998
DEFINITION	Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
ACCESSION	U57560
VERSION	U57560.1 GI:1575067
KEYWORDS	
SOURCE	Macaca mulatta
ORGANISM	Macaca mulatta
REFERENCE	
AUTHORS	Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A. and Capra, J.D.
TITLE	Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL	Mol. Immunol. 34 (3), 237-253 (1997)
MEDLINE	97368199
REFERENCE	2 (bases 1 to 420)
AUTHORS	Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.

[illegible]



U57563	GI:1575073
VERSION	
KEYWORDS	
SOURCE	rhesus monkey.
ORGANISM	Macaca mulatta
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
AUTHORS	1 (bases 1 to 411) Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.
TITLE	Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
JOURNAL	MoI. Immunol. 34 (3), 237-253 (1997)
MEDLINE	97368199
AUTHORS	2 (bases 1 to 411) Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A. and Capra,J.D.
TITLE	Direct Submission
JOURNAL	Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
FEATURES	Location/Qualifiers 1..411 /organism="Macaca mulatta" /db_xref="taxon:9544" /note="hybridoma 1B4" 1..>411 /codon_start=1 /product="immunoglobulin heavy chain" /protein_id="AAC02640.1" /db_xref="GI:1575074"
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BASE COUNT	81 a 124 c 115 g 91 t
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Query Match	75.2%; Score 318.2; DB 9; Length 411;
Best Local Similarity	88.2%; Pred. No. 5.4e-77;
Matches	373; Conservative 0; Mismatches 38; Indels 12; Gaps 2;
Qy	1 ATGAACACCTGTGGTCTCTCCTCCTGTGTGCAGCTCCAGATGGTGCTGTGCCAG 60
Db	1 ATGAACACCTGTGGTCTCTCCTCCTGTGTGCAGCTCCAGATGGTGCTGTGCCAG 60
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Db	61 GTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCAAC 120
Qy	121 TGCCTGTCTCTGTGGCTCTGTACAGAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
Db	121 TGCCTGTCTCTGTGGCTC---CATCAGCAGTAACTGGTGGACCTGGATCCGCCAGCCC 177
Qy	181 CCAGGAAGGACCTGGAGTGGAGTATCTCTGTGTGTGGTGGTGGGCCACCAACTAC 240
Db	178 CCAGGAAGGACCTGGAGTGGATGGATTTGAGCTTCTATGGTACTAGTGGGAGCACTACTAT 237
Qy	241 AACCCGTCCTTCAGAGTCGAGTCATCATTTCAAGACACGTCCTCAAGAACCACTTCTCC 300
Db	238 AACCCCTCCCTCAGGTCGAGTCACCATTTCAACAGACACGTCCTCAAGAACCACTTCTCC 297
Qy	301 CTGAACCTGAACCTCTGTACCGCCCGGACACGCGCGTGTATTACTGTGCCAGAGATTGG 360
Db	298 CTGAAGCTGAGCTCTGTACCGCCCGGACACGCGCGTGTATTACTGTGCCAGGAT--- 354
Qy	361 GCCCAATATGCTGGAACAACGCTAGGCTTCTTGGGGCCAGGGAGTCTGGTCAACCGTCTCC 420
Db	355 -----ACAGTAAGTAAGCCCTTTGACTACTTGGGGCCAGGGAGTCTGGTCAACCGTCTCC 408
Qy	421 TCA 423

Qy	301	CTGAACCTGAACTCTGTGACC	CGCGGCAGACACGGCCGTGTATTACTGTGCAGAGATTGG	360
Db	298	CTGAAGTGTAGCTCTGTGAC	CGCGGCAGACACGGCCGTGTATTACTGTGCAGAGATTGG	357
Qy	361	GCCCAATAGTCG--	--AACAACCTAGGCTTCTGGGGCCAGGAGTCTTGTCACCGTC	417
Db	358	GGATTTTGGAGTGGTATC	TCTTTGACTACTTGGGGCCAGGAACCTTGTCACCGTC	417
Qy	418	TCCTCA	423	
Db	418	TCCTCA	423	
RESULT	5			
MMU57568				
LOCUS				
DEFINITION		MMU57568	414 bp mRNA linear	PRI 11-FEB-1998
ACCESSION			Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC	
VERSION		U57568	antibody, mRNA, partial cds.	
KEYWORDS				
SOURCE		U57568.1	GI:1575083	
ORGANISM			rhesus monkey.	
REFERENCE			Macaca mulatta	
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE			Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;	
JOURNAL			Cercopithecinae; Macaca.	
MEDLINE			1 (bases 1 to 414)	
REFERENCE			Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F.,	
AUTHORS			Blancher,A. and Capra,J.D.	
TITLE			Variable region gene segment utilization in rhesus monkey	
JOURNAL			hybridomas producing human red blood cell-specific antibodies:	
MEDLINE			predominance of the VH4 family but not VH4-21 (V4-34)	
REFERENCE			MoI. Immunol. 34 (3), 237-253 (1997)	
AUTHORS			97368199	
TITLE			2 (bases 1 to 414)	
JOURNAL			Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.	
MEDLINE			and Capra,J.D.	
REFERENCE			Direct Submission	
AUTHORS			Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,	
TITLE			University of Texas Southwestern Medical Center, 6000 Harry Hines	
JOURNAL			Bldv., Dallas, TX 75235-9140, USA	
FEATURES			Location/Qualifiers	
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BASE COUNT			83 a 128 c 110 g	
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Query Match			74.4%; Score 314.6; DB 9; Length 414;	
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Matches			370; Conservative 0; Mismatches 44; Indels 9; Gaps 2;	
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Db	1	ATGAACACCTGTGGTTCCTCT	CCTCCTCGTGGTGGCACCTCCCAGATGGGTCGTGCCAG	60
Qy	61	CTGCAGCTGCAGGAGTCGG	CGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTCACC	120
Db	61	GTGCAGCTGCAGGAGTCGG	CGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTCACC	120
Qy	121	TGGCTCTCTCTGTGGTCT	GTGTGACAGTAGTAACCTGGTGGACCTGGATCCGCGCACC	180

Db	121	TCGCGTCTCTGTTTACTC---CATCAGCAGTAACACTACTGGAGCTGGATCGGCCAGCC	177			
Qy	181	CCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGTAGTGGTGGGCCACCAACTAC	240			
Db	178	CCAGGGAAGGACTGGAGTGGATTGGCTATATCTATGTAGTAGTGGAGCGCCTACTAC	237			
Qy	241	AACCGTGCCCTCAAGAGTCGAGTCATCATTTCAACAGACACAGCTCCAGAACCACTTCTCC	300			
Db	238	AACCCCTCCCTCAAGAGTCGAGTCACGATTTCAATAGACACAGTCCAAGAACCACTTCTCC	297			
Qy	301	CTGAACCTGAACTCTGTACCGCGCGACACGCGCTGTATTACTGTGCAGAGATTGG	360			
Db	298	CTGAAGCTGAGCTCTGTACCGCGCGACACGCGCTCTATTACTGTGCAGAGATT---	354			
Qy	361	GCCCAATAGCTGGAACAACGCTAGGCTTCGTGGGCCAGGAGTCTGTGTACCGTCTCC	420			
Db	355	---CCCTACGGTCCACATACTTTGACTACTTGGGCCAGGAGTCTGTGTACCGTCTCC	411			
Qy	421	TCA 423				
Db	412	TCA 414				
RESULT 6						
AR108867						
LOCUS	AR108867	1431 bp	DNA linear PAT 14-FEB-2001			
DEFINITION	Sequence 11 from patent US 6113898.					
ACCESSION	AR108867					
VERSION	AR108867.1 GI:12825143					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1431)					
AUTHORS	Anderson,D.R., Brams,P., Hanna,N., Shestowsky,W.S. and Heard,C.					
TITLE	Human B7.1-specific primatized antibodies and transfectomas					
JOURNAL	expressing said antibodies					
FEATURES	Patent: US 6113898-A 11 05-SEP-2000;					
source	Location/Qualifiers					
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BASE COUNT	319 a	462 c	385 g 265 t			
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Query Match 74.0%; Score 313.2; DB 6; Length 1431;						
Best Local Similarity 84.5%; Pred. No. 1.3e-75;						
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;						
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Db	1	ATGAACACCTGTGGTTCTTCCTCCTCTGTGGCAGCTCCAGATGGTCTGTCCCGAG	60			
Qy	61	CTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCAC	120			
Db	61	GTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCAC	120			
Qy	121	TGCCTCTCTCTGTGGTCTGTGCAGCAGTAGTAACCTGTGGACCTGGATCCGCCAGCC	180			
Db	121	TGCCTCTCTCTGTGGTCTGCATCAGCGGTGGTTATGGCTGGGCTGGATCCGCCAGCC	180			
Qy	181	CCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC	240			
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Db	241	AACCCCTCCCTCAAGAGTCAAGTCACCATTTCAACAGACACGCTCCAGAACCACTTCTCC	300			
Qy	301	CTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCAGAGATTGG	360			
Db	301	CTGAAGCTGAACCTATTAGACCGCGGACACGCGCGTGTATTACTGTGTGAGAGATCGT	360			

QY	361	GCCCAATAGCTGCANCA	-----CCCTAGGCTTCTGGGGCCAGGGAGTC	405
Db	361	CTTTTTCAGTGTTCGAATGTTACAAACA	CTGTCGATGCTGGGGCCGGGAGTC	420
QY	406	CTGGTCACCGTCTCCCTCA	423	
Db	421	CTGGTCACCGTCTCCCTCA	438	

RESULT	7		
AF062120			
LOCUS	AF062120	426 bp	mRNA
DEFINITION	Homo sapiens clone 21u-39 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.		
			PRI 08-MAY-2001

ACCESSION AF062120  
VERSION AF062120.1 GI:3170702  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 426)  
AUTHORS Wang, X. and Stollar, B. D.  
TITLE Immunoglobulin VH gene expression in human aging  
JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)

MEDLINE	99459182
PUBMED	10527689
REFERENCE	2 (bases 1 to 426)
AUTHORS	Wang,X. and Stollner,B.D.
TITLE	Direct Submission
JOURNAL	Submitted (22-APR-1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES	Location/Qualifiers
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Query Match	73.9%	Score 312.4;	DB 9;	Length 426;
Best Local Similarity	86.6%	Pred. No. 2.1e-75;		
Matches 369; Conservative		0; Mismatches 51;	Indels 6;	Gaps 2;

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Qy	61 CTGCAGCTGCAGGAGTCGGGGCCAGGAGTGGTGAAGCTTCGGAGACCTGTCCCTCACC	120
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[illegible]

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RESULT 8

HSIGHXX25	LOCUS	DEFINITION	420 bp	mRNA	linear	PRI 26-JUL-1997
HSIGHXX25	LOCUS	H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-5).				

ACCESSION X65907 S58702  
 VERSION X65907.1 GI:395105  
 KEYWORDS diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.

SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE  
1 (bases 1 to 420)

**AUTHORS** Schiff, C.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE

REFERENCE  
2 (bases 1 to 420)  
AUTHORS  
Miliu, M., Le Deist, F., de Saint-Basile, G., Fischer, A.,  
Fougereau, M. and Schiff, C.  
TITLE  
Bone marrow cells in X-linked agammaglobulinemia express  
pre-B-specific genes (lambda-light and V pre-B) and present

JOURNAL  
MEDLINE  
J. Clin. Invest. 91 (4), 1616-1629 (1993)  
repetoire  
93232287

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ORIGIN

Query Match	73.5%	Score 311;	DB 9;	Length 420;
Best Local Similarity	85.1%			
		Prod No	5	26-75;

DEPT DOCUMENTS DIVISION      REC. NO. 3-25 751

Matches 360; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 1 ATGAACACACTGTGGTCTCTCTCCCTCCCTGGTGGCAGCTCCACAGATGGGTCTGTCTCCAG 60  
|||||  
Db 1 ATGAACACACTGTGGTCTCTCTCCCTCCCTGGTGGCAGCTCCACAGATGGGTCTGTCTCAG 60  
|||||

QY 61 CTCAGCTGCAGAGTCGGGCCAGGAGTGGTGAACCTTCGGAGACCCCTGTCCTTCACC 120  
|||||  
Db 61 CTCAGCTGCAGAGTCGGGCCAGGAGTGGTGAACCTTCGGAGACCCCTGTCCTTCACC 120  
|||||

QY 121 TGGGCTGTCTCTGGTGGCTCTGTGCACAGTAGTAACCTGTGGACCTGGATCCGCCAGCCC 180  
|||||  
Db 121 TGGGCTGTCTCTGGTGGCTCTGTGCACAGTAGTAACCTGTGGACCTGGATCCGCCAGCCC 180  
|||||

QY 181 CCAGGAAGGAGTGGAGTGGATTTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTAC 240  
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Db 181 CCAGGAAGGAGTGGAGTGGATTTGGGAATCAATCATAGTGGAG---CACCAACTAC 237  
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QY 241 AACCCGTCCCTCAAGAGTCGAGTCATCATTTCCACAGACACGTCCCAAGAACCAAGTTCTCC 300  
|||||  
Db 238 AACCCGTCCCTCAAGAGTCGAGTCATCATTTCCACAGACACGTCCCAAGAACCAAGTTCTCC 297  
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QY 301 CTGAACCTGAACCTCTGTGACCGCCGGGACACGGCGGTGTATTACTGTCCAGAGATTGG 360  
|||||  
Db 298 CTGAACCTGAACCTCTGTGACCGCCGGGACACGGCGGTGTATTACTGTCCAGAGATTGG 357  
|||||

QY 361 GCCAAATAGCTGGAACACAGCTAGCTTCTGGGGCCAGGAGTCTGTGTCACCGTCTCC 420  
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Db 358 CCGGGGAGTACTACTACTACGTATGGACGTCTGGGGCCAGGACACCGTCTACCGTCTCC 417  
|||||

QY 421 TCA 423  
|||

Db 418 TCA 420  
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RESULT 9

HUMIGHZF HUMIGHZF 420 bp mRNA linear PRI 09-NOV-1994

LOCUS Human (clone R5A3H) Ig rearranged H-chain mRNA V-region, 5' end.

DEFINITION M99607

ACCESSION M99607

VERSION 1

KEYWORDS V-region; complementarity determining region; immunoglobulin heavy chain; processed gene.

SOURCE Homo sapiens female adult blood cDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 420)

AUTHORS Weng,N.P., Yu-Lee,I.Y., Sanz,I., Patten,B.M. and Marcus,D.M.

TITLE Structure and specificities of anti-ganglioside autoantibodies associated with motor neuropathies

JOURNAL J. Immunol. 149 (7), 2518-2529 (1992)

MEDLINE 92407350

FEATURES

Location/Qualifiers

1..420

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/db\_xref="taxon:9606"

/map="14q32.33"

/sex="female"

/cell\_type="B lymphocytes"

/tissue\_type="blood"

/dev\_stage="adult"

1..420

/gene="IGHV"

1..57

/gene="IGHV"

/note="G00-128-528"

1..>420

/gene="IGHV"

/codon\_start=1

/product="immunoglobulin heavy chain"

/protein\_id="AAA52982.1"

/db\_xref="GI:185496"

gene

sig\_peptide

CDS

/db\_xref="GDB:G00-128-528"

/translation="MKHLFFLLVAAPRWLSQLQLOESGPGLVKPSSETLSLCTVSGSISSEFYWGIWIRPPGKGLIEWIGSIYSGSTYINPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVVYCARSPRIVGANKDVWGQGTIVTVSS"

58..420

/gene="IGHV"

/note="G00-128-528"

148..165

/gene="IGHV"

/standard\_name="CDR-1"

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208..286

/gene="IGHV"

/standard\_name="CDR-2"

/note="G00-128-528"

352..387

/gene="IGHV"

/standard\_name="CDR-3"

/note="G00-128-528"

BASE COUNT 81 a 126 c 121 g 92 t

ORIGIN

Query Match 73.3%; Score 310; DB 9; Length 420;

Best Local Similarity 85.1%; Pred. No. 9.8e-75;

Matches 359; Conservative 0; Mismatches 60; Indels 3; Gaps 1;

QY 1 ATGAACACACTGTGTCCAG 60  
|||||  
Db 1 ATGAACACACTGTGTCCAG 60  
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QY 61 CTCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTCTCCCTCACC 120  
|||||  
Db 61 CTCAGCTGCAGAGTCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTCTCCCTCACC 120  
|||||

QY 121 TCGGCTGTCTCTGTGGTCTCTCTCAGCAGTAGTACTGTGTGACCTGGATTCGCCAGCCCC 180  
|||||  
Db 121 TCGACTGTCTCTGTGGTCTCTCAGCAGTAGTACTGTGTGACCTGGATTCGCCAGCCCC 180  
|||||

QY 181 CCAGGAAGGAGTGGAGTGGATTTGGACGTATCTCTGGTAGTGGTGGGCCACCAACTAC 240  
|||||  
Db 181 CCAGGAAGGAGTGGAGTGGATTTGGAGTATCTATTATA---GTGGAGACCTACTACTAC 237  
|||||

QY 241 AACCCGTCCCTCAAGAGTCGAGTCATCATTTCCACAGACACGTCCCAAGAACCAAGTTCTCC 300  
|||||  
Db 238 AACCCGTCCCTCAAGAGTCGAGTCATCATTTCCAGACACGTCCCAAGAACCAAGTTCTCC 297  
|||||

QY 301 CTGAACCTGAACCTCTGTGACCGCCGGGACACGGCGGTGTATTACTGTCCAGAGATTGG 360  
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Db 298 CTGAAGCTGAGCTGTGTGACCGCCGTGACACGGCTGTATTACTGTGCGAGACGGTCT 357  
|||||

QY 361 GCCAAATAGCTGGAACACAGCTAGCTTCTGGGGCCAGGAGTCTGTGTCACCGTCTCC 420  
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Db 358 CCGGGGAGTACTACTACTACGTATGGACGTCTGGGGCCAGGACACCGTCTACCGTCTCC 417  
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QY 421 TC 422  
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Db 418 TC 419  
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RESULT 10

HUMIGHZF HUMIGHZF 468 bp mRNA linear PRI 27-JUL-1994

LOCUS Human immunoglobulin heavy chain variable region (VH IV family)

DEFINITION from IgM rheumatoid factor.

ACCESSION L29122

VERSION L29122.1

KEYWORDS Ig heavy chain; rheumatoid factor; variable region subgroup VH-IV.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 468)

AUTHORS	Fang, Q., Kannapell, C. C., Gaskin, F., Solomon, A., Koopman, W. J. and Fu, S. M.
TITLE	Human rheumatoid factors with restrictive specificity for rabbit immunoglobulin G: auto- and multi-reactivity, diverse VH gene segment usage and preferential usage of V lambda IIIB
JOURNAL	J. Exp. Med. 179, 1445-1456 (1994)
MEDLINE	94216813
FEATURES	Location/Qualifiers 1..468 /organism="Homo sapiens" /db_xref="taxon:9606" /map="14q32.33" /cell_line="KES 643" /cell_type="non-T" /tissue_type="peripheral blood" 1..468 /gene="IGH@" <38..>468 /gene="IGH@" /codon_start=1 /product="immunoglobulin heavy chain VDJ region" /protein_id="AAA20138.1" /db_xref="GI:465145" /translation="MKHLWFFLLVAAPRWLSOVLOESGCLVKPSTLSLTCAVSGSISNNWWSVRPPGKGLWIGELIYHSSTNYPNLSKRVITISVDKSKNQFSLKLSSTVADTAVIYCARCHSSSWAFDWMGQGLTLTVSSGSASAP" 39 a 138 c 139 g 98 t
BASE COUNT	93 a 138 c 139 g 98 t
ORIGIN	
Query Match	73.2%; Score 309.8; DB 9; Length 468;
Best Local Similarity	86.8%; Pred. No. 1.1e-74;
Matches	367; Conservative 0; Mismatches 47; Indels 9; Gaps 2;
QY	1 ATGAACACCTGTGGTCTCTCCTCCTCGTGGCAGCTCCAGATGGTCTGTCCAG 60       Db
QY	38 ATGAACACCTGTGGTCTCTCCTCCTCGTGGCAGCTCCAGATGGTCTGTCTAG 97       Db
QY	61 CTGCAGCTGCAGGAGTCGGCCCGCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCAC 120       Db
QY	98 GTGCAGCTGCAGGAGTCGGCCCGCAGGAGTGGTGAAGCCTTCGGGAGCCCTGTCCCTCAC 157       QY
QY	121 TGGCCTCTCTCTGGTGGCTCTGTGACGAGTAGTAACCTGGTGGACCTGGATCGCGCAGCCC 180       Db
QY	158 TGGCCTCTCTCTGGTGGCTCCATCAGCAGTAGTAACCTGGTGGAGTTGGGTCCGCGCAGCCC 217       QY
QY	181 CCAGGGAAGGAGCTGGAGTGGATTGGAGCTATCTCTGGTAGTGGTGGGCGCACCAACTAC 240       Db
QY	218 CCAGGGAAGGAGCTGGAGTGGATTGGGGAATCTATCATATA---GTGGGAGCAACCAACTAC 274       QY
QY	241 AACCCGTCCCTCAAGAGTCAGAGTCATCATTTTCAAGACACAGCTCAAGAACCAAGTCTCTCC 300       Db
QY	275 AACCCGTCCCTCAAGAGTCAGAGTCACCATATCAGTAGACAAGTCCAGAACCAAGTCTCTCC 334       QY
QY	301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCTGTATTACTGTGCAGAGATTGG 360       Db
QY	335 CTGAAGCTGAGCTGTGTGACCGCGCGGACACGCGCTGTATTACTGTGCAGAGTCTCTCC 388       QY
QY	361 GCCCAATAGCTGGAACAAAGCTAGGCTTCTGGGGCCAGGAGTCCCTGGTACCGTCTCC 420       Db
QY	389 GGGCATAGCAGCAGCTGGGCGTTTGACTACTTGGGGCCAGGGAACCTTGGTACCGTCTCC 448       QY
QY	421 TCA 423       Db
QY	449 TCA 451
RESULT 11	
HST22X26	
LOCUS	HST22X26 414 bp mRNA linear PRI 30-APR-1997
DEFINITION	H. sapiens mRNA for Ig heavy chain variable region (VH4DJ) (clone T22.26).
ACCESSION	275399









GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:06:45 ; Search time 3874.81 Seconds  
(without alignments)  
1473.417 Million cell updates/sec

Title: US-09-019-441-2  
Perfect score: 423  
Sequence: 1 ATGAACACCTGTGGTCTT.....TCCTGGTCACCGTCTCTCTCA 423

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_gss.\*
- 13: em\_gss\_hum.\*
- 14: em\_gss\_inv.\*
- 15: em\_gss\_pln.\*
- 16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	301.6	71.3	453	9	AW402337 UI-HF-BK0
2	301.4	71.3	862	10	BG397580 602438620
3	299	70.7	867	10	BG685428 602637281
4	290.2	68.6	798	10	BI771905 603058919
5	290	68.6	968	9	AL552672 AL552672
6	288.4	68.2	850	10	BG686474 602637417
7	288.2	68.1	939	9	AL541900 AL541900
8	285.4	67.5	820	10	BI770055 603053578
9	285	67.4	680	10	BG684306 602636046
10	283.2	67.0	814	10	BG685325 602637556
11	281	66.4	736	10	BG685592 602637569
12	280.6	66.3	648	10	BM008069 603617839
13	280.4	66.3	643	9	AUI34293 AUI34293
14	280	66.2	729	10	BG548421 602575006
15	279.6	66.1	570	10	BG684621 602636395
16	279.6	66.1	894	10	BG757611 602714787
17	279.4	66.1	959	10	BG757666 602711256

18	279	66.0	633	10	BG685695
19	278.6	65.9	661	10	BG686421
20	278.4	65.8	416	10	BG757951
21	277.8	65.7	948	10	BM007780
22	277.6	65.6	971	9	AL560682
23	277.4	65.6	632	10	BG341565
24	276.4	65.3	828	10	BF974568
25	276	65.2	980	10	BG684861
26	274.8	65.0	924	10	BG758027
27	273.4	64.6	524	10	BG684700
28	271.8	64.3	733	10	BM008087
29	270.8	64.0	889	10	BG758751
30	270.4	63.9	832	9	AUI22174
31	269.4	63.7	1097	10	BF974768
32	269.2	63.6	558	10	BM007652
33	269	63.6	649	10	BG757507
34	268.6	63.5	841	10	BG397667
35	268.4	63.5	742	10	BG745613
36	267.8	63.3	791	10	BG685529
37	267.4	63.2	721	10	BG686995
38	267.4	63.2	937	10	BF663511
39	267	63.1	509	9	AW406349
40	267	63.1	834	10	BG758193
41	266.8	63.1	863	10	BM007811
42	266.4	63.0	809	10	BG685383
43	266.2	62.9	803	10	BG397978
44	265.8	62.8	844	10	BI489640
45	265.2	62.7	859	10	BG757166

## ALIGNMENTS

RESULT 1

AW402337

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW402337 453 bp mRNA linear EST 16-FEB-2000  
UI-HF-BK0-aal-g-02-0-UI.rl NIH\_MGC\_35 Homo sapiens cDNA clone  
IMAGE:3053955 5', mRNA sequence.  
AW402337  
AW402337.1 GI:6921023  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.  
Location/Qualifiers  
1..453  
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/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LT1)"  
/note="Vector: pT73-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(0.5-1.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonafido, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 88 a 145 c 129 g 91 t

Query Match 71.3%; Score 301.6; DB 9; Length 453;  
Best Local Similarity 86.9%; Pred. No. 6.9e-68;  
Matches 344; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

QY 28 CTGGTGGACGCTCCAGATGGGCTGCTCCAGCTCCAGCTCCAGAGTCGGGCCAGGA 87  
Db 8 CTGGTGGACGCTCCAGATGGGCTGCTCCAGGTCAGCTCCAGAGTCGGGCCAGGA 67  
QY 88 GTGGTGAAGCCTTCGGAGACCTGTCCCTCACCTGGCTGTCTCTGGTGGCTGTGTCACG 147  
Db 68 GTGGTGAAGCCTTCGGAGACCTGTCCCTCACCTGGCTGTCTCTGGTGGCTGTGTCACG 127  
QY 148 AGTAGTAACCTGGTGGACCTGGATTCGCCAGCCGCCAGGGAAGGAGCTGGAGTGGATTGA 207  
Db 128 AGTGGTTACTCTCTGGGCTGGATTCGGCAGCCGCCAGGGAAGGAGCTGGAGTGGATTGG 187  
QY 208 CGTATCTCTGGTAGTGGTGGGCCACCACTACACCCCTCCCTCAAGAGTCGAGTCATC 267  
Db 188 AGTATCTATCATCA---GTGGGAGCAGCTACTACACCCCTCCCTCAAGAGTCGAGTCAC 244  
QY 268 ATTTCACAGACAGCTCCAGAACCTGCTCCCTGAACCTGAACCTGCTGACCCGCCGG 327  
Db 245 ATATCAGTAGACAGCTCCAGAACCTGCTCCCTGAACCTGCTGACCCGCCGG 304  
QY 328 GACACGGCGGTATTTACTGTGCGAGAGATTGGGCCAAATAGCTGGACACAGCTAGGC 387  
Db 305 GACACGGCGGTATTTACTGTGCGAGACATACGGGCTATATAGTGGGTACCCCTTTGAC 364  
QY 388 TTCTGGGGCCAGGAGTCTCTGTGTCACCGTCTCTCA 423  
Db 365 TACTGGGGCCAGGACCTGTGTCACCGTCTCTCA 400

RESULT 2  
BG397580  
LOCUS 602438620F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4565020 5',  
DEFINITION mRNA sequence.  
ACCESSION BG397580  
VERSION BG397580.1 GI:13291028  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 862)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

plate: LCM1281 row: g column: 05  
High quality sequence stop: 827.  
Location/Qualifiers

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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
Site:2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."  
BASE COUNT 210 a 262 c 244 g 146 t  
ORIGIN

Query Match 71.3%; Score 301.4; DB 10; Length 862;  
Best Local Similarity 85.3%; Pred. No. 1e-67; 56; Indels 6; Gaps 2;  
Matches 361; Conservative 0; Mismatches 56; Indels 6; Gaps 2;

QY 1 ATGAACACCTGTGGTTCTCTCTCTGGTGGCAGCTCCAGATGGTCTGTCTCCACG 60  
Db 23 ATGAACACCTGTGGTTCTCTCTCTGGTGGCAGCTCCAGATGGTCTGTCTCAG 82  
QY 61 CTCGAGCTCGAGAGTCGGGCCCGGAGGTGGTGAAGCTTCGGAGACCTGTCTCCAC 120  
Db 83 CTCGAGCTCGAGAGTCGGGCCCGGAGGTGGTGAAGCTTCGGAGACCTGTCTCCAC 142  
QY 121 TCGGCTGTCTCTGGTGGCTGTGTACAGCTAGTAACTGTGACCTGGATCCGCCAGCCC 180  
Db 143 TCGGCTGTCTCTGGTGGCTGTGTACAGCTAGTAACTGTGAGTGGTTCGCCAGCCC 202  
QY 181 CCAGGGAAGGAGCTGGAGTGGATTTGACCTATCTCTGTGTGGTGGGCCACCAACTAC 240  
Db 203 CCAGGGAAGGAGCTGGAGTGGATTTGAGAAATCTATCATA---GTGGGAGCAACTAC 259  
QY 241 AACCCGTCCTCAAGAGTCGAGTCATCTTTCACAGACACCTCCAGAACCACTCTCC 300  
Db 260 AACCCGTCCTCAAGAGTCGAGTCATCTTTCACAGACACCTCCAGAACCACTCTCC 319  
QY 301 CTGAACCTGAACCTGTGTACCCGCCGACGCGGTATTACTGTGCCAGAGATTGG 360  
Db 320 CTGAACCTGAACCTGTGTACCCGCCGACGCGGTATTACTGTGCCAG---TCTG 376  
QY 361 GCCCAATAGCTGGAAACACGCTAGCTTCTGGGCCAGGAGTCTGTGTACCGTCTCC 420  
Db 377 GGAGACATCTACTACTACGGTATGAGACGCTCTGGGCCAAGGAGGACCGTCTCC 436  
QY 421 TCA 423  
Db 437 TCA 439

RESULT 3

BG685428  
LOCUS 602637281F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4764956 5',  
DEFINITION mRNA sequence.  
ACCESSION BG685428  
VERSION BG685428.1 GI:13916825  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 867)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.



Db 369 ---GTGACACGGCTCGATATAAACTGGAGCTCTGGGGCCAAGGACCAACGGTCCACGGTC 425

Qy 418 TCCTCA 423  
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Db 426 TCCTCA 431

RESULT 6

LOCUS BG686474

DEFINITION 602637417F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4764965 5', mRNA sequence.

ACCESSION BG686474

VERSION BG686474.1 GI:13917871

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 850)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCMI623 row: b column: 06  
High quality sequence stop: 759.

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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pGB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH\_MGC Library."

BASE COUNT 186 a 265 c 229 g 170 t

ORIGIN

Query Match 68.2%; Score 288.4; DB 10; Length 850;  
Best Local Similarity 84.9%; Pseq No. 2 4e-64;  
Matches 348; Conservative 0; Mismatches 56; Indels 6; Gaps 2;

Qy 1 ATGAACACCTGTGGTTCTTCCTCCTCCTGTGTGCAGCTCCAGATGGGTCTGTCCACG 60  
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Db 23 ATGAACATCTGTGGTTCTTCCTCCTCCTGTGTGCAGCTCCAGATGGGTCTGTCCACG 82  
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Qy 61 CTGCAGCTGCAGGAGTCGGGCCACGAGTGTGAAGCTTCGGAGACCTGTCCCTCACC 120  
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Db 83 GTGCAGCTGCAGGAGTCGGGCCACGAGTGTGAAGCTTCACAGACCTGTCCCTCACC 142  
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Qy 121 TGCCTGTCTCTGGTGGCTCTGTTCAGCA--GAGTAACCTGGTCGACCTGGATCGGCAC 177  
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Db 143 TGCAGCTGTCTGTGGTGGCTTCATCAGCAGTGGTAGTTACTACTGGAGCTGGATCGGCAG 202  
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Qy 178 CCCCCAGGAGGACCTGGAGTGGATTGGAGCATCTCTCTGTGTGGTGGGGCCACCAAC 237  
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RESULT 5
AL552672 AL552672 968 bp mRNA linear EST 16-FEB-2001
LOCUS LTI_NFL006.PL2 Homo sapiens cDNA clone CS0DI067YK24 5
DEFINITION prime, mRNA sequence.
ACCESSION AL552672.1 GI:12891798
VERSION AL552672
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 968)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE Li, W.B., Gruber, C., Jessée, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI067YK24"
/clone_lib="LTI_NFL006.PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 201 a 327 c 256 g 179 t 5 others
ORIGIN

Query Match 68.68; Score 290; DB 9; Length 968;
Best Local Similarity 85.08; Pred. No. 9.8e-65;
Matches 362; Conservative 1; Mismatches 51; Indels 12; Gaps 3;

Qy 1 ATGAACACCTGTGGTCTCTCCTCCTCGTGTGCAGCTCCACAGATGGTCTCTGCCAG 60
Db 15 ATGAAGCACCTGTGGTCTCTCCTCCTCGTGTGGCGCTCCAGATGGTCTCTGCCAG 74

Qy 61 CTGCAGCTGCAGGAGTCGGGCCACGAGAGTGGTGAAGCTTCGGAGACCTCTGCCCTCAC 120
Db 75 CTGCAACTGCAGGAGTCGGGCCACGAGACTGGTGAAGCTTCGGAGACCTCTGCCCTCAC 134

Qy 121 TGCCTCTCTCTGTGGCTCTGTCTCAGCAGTAGTA---ACTGGTGGACCTGGATCGGCAG 177
Db 135 TGCACCTGTCTCTGTGGCTTCATCAGCAGTAGTAGTACTACTGGGCTGGATCGGCAG 194

Qy 178 CCCCAGGAAGGACCTGGAGTGGATTGGACCTATCTCTGGTACTGGTGGGGCCCAACAA 237
Db 195 CCCCAGGAAGGGCTGGAGTGGATTGGAGTATCTATTATA---GTGGAGGACCCAC 251

Qy 238 TACAACCGTCCCTCAAGAGTCGAGTCATCATTTTCAACAAGACACGTCACAAGACGATTC 297
Db 252 TACAACCGTCCCTCAAGAGTCGAGTCACCATATATCAAGAAGACACGTCACAACGATTC 311

Qy 298 TCCCTGAACCTGAACCTCTGTGACCGCCGCGACACGCCGTGTATTACTGTGCCAGAGAT 357
Db 312 TCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGA--- 368

Qy 358 TGGGCCCAAAATAGCTGGAAACAACGCTAGGCTTCTTGGGGCCAGGGAGTCTTGTTCCACGTC 417

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Db 203 CCGCGGGAAGGACTGGAGTGGATTGGCGGTATCT---ATACCAGTGGGACCAAC 259
QY 238 TACAACCCCTCCCTCAAGAGTCAGTCATATTTCACAAGACACAGTCCCAAGAACCAAGTTC 297
Db 260 TACAACCCCTCCCTCAAGAGTCAGTCATATTTCACAAGACACAGTCCCAAGAACCAAGTTC 319
QY 298 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCCAGAT 357
Db 320 TCCCTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCCAGAGGA 379
QY 358 TGGGCGCAATAGCTGGAACAACAGCTAGCTTCTTGGGGCCAGGAGTCCCT 407
Db 380 AGTCTCTTATGCTACATAATTACGTTTGTGGAAAGCTCGCGGAGCCCT 429

RESULT 7
AL541900
LOCUS
DEFINITION AL541900 LFI_FL002_PL1 939 bp mRNA linear EST 16-FEB-2001
            ' mRNA sequence.
ACCESSION AL541900
VERSION    AL541900.1 GI:12873414
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE    Full-length cDNA libraries and normalization
JOURNAL  Unpublished (2001)
COMMENT  Contact: Genoscope
          Genoscope - Centre National de Sequencage
          BP 191 91006 EVRY cedex - France
          Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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             /organism="Homo sapiens"
             /db_xref="taxon:9606"
             /clone="CS0DE007YL07"
             /lab_host="LTI_FL002_PL1"
             /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
             cDNA was primed with a NotI-oligo(dT) primer. Five prime
             end enriched, double-stranded cDNA was digested with Not I
             and cloned into the Not I and Eco RV sites of the
             pCMVSPORT 6 vector. Library was constructed by Life
             Technologies. Contact : Feng Liang Life Technologies, a
             division of Invitrogen 9800 Medical Center Drive Rockville
             Maryland 20850, USA Fax : (1) 301 610 8371 Email :
             fliang@lifetech.com URL :
             http://fulllength.invitrogen.com"
BASE COUNT 195 a 324 c 243 g 176 t 1 others
ORIGIN

Query Match 68.1%; Score 288.2; DB 9; Length 939;
Best Local Similarity 86.0%; Pred. No. 2.8e-64;
Matches 369; Conservative 0; Mismatches 48; Indels 12; Gaps 4;

QY 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGCAGCTCCCAAGATGGGTCTGTCCCGAG 60
Db 13 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGCAGCTCCCAAGATGGGTCTGTCCCGAG 72
QY 61 CTGACGTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGAGACCCCTGTCCCTCAC 120
Db 73 GTGACGTGCAGGAGTCGGGCGCCAGGAGTGGTGAAGCCTTCGAGACCCCTGTCCCTCAC 132
QY 121 TGGCGTGTCTGTGGTGGCTCTGTGCAGCAGTAGTAAGTGTGGACCTGGATCCCGCAGCCC 180
Db 133 TGCACGTGTCTGTGGCTC---CATCAGTAGTACTACTGGAGCTGGATCCCGCAGCCC 189
QY 181 CCAGGGAAGGACTGGAGTGGATTGGACGTATCTCTGTGTAGTGGTGGGCGCCCAACTAC 240

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Db 190 GCGGGAAGGACTGGAGTGGATTGGCGGTATAT---ATATAGTGGGACCAACTAC 246
QY 241 AACCCGTCCTCCCTCAAGAGTCAGTCATATTTCACAAGACACAGTCCCAAGAACCAAGTTC 300
Db 247 AACCCGTCCTCCCTCAAGAGTCAGTCATATTTCACAAGACACAGTCCCAAGAACCAAGTTC 306
QY 301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCCAGA---GA 356
Db 307 CTGAAGCTGACCTCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGCCAGAGTGT 366
QY 357 TTGGGCGCAATAGCTGGAACAACAGCTA--GGCTTCTGGGGCCAGGAGTCTCTGGTGCACC 414
Db 367 TTTTGGACTGATACCTACTACTACTAGGTATGGAGCTGTGGGGCCAGGACCGGTCACC 426
QY 415 GTCTCCTCA 423
Db 427 GTCTCCTCA 435

RESULT 8
BI770055
LOCUS
DEFINITION 603053578F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203338 5',
            mRNA sequence.
ACCESSION BI770055
VERSION    BI770055.1 GI:15761633
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM1509 row: k column: 19
          High quality sequence start: 16
          High quality sequence stop: 797.

FEATURES
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             /db_xref="taxon:9606"
             /clone="IMAGE:5203338"
             /clone_lib="NIH_MGC_122"
             /lab_host="DH10B"
             /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
             Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
             anonymous pool of 24 week female lung, 16 week female
             spleen, and 20-22 week male spleens. Library is oligo-dT
             primed and directionally cloned (EcoRV site is destroyed
             upon cloning). Average insert size 1.4 kb, insert size
             range 1-3 kb. Library is normalized and enriched for
             full-length clones and was constructed by C. Gruber
             (Invitrogen). Research Genetics tracking code 026. Note:
             this is a NIH_MGC Library."
BASE COUNT 175 a 252 c 218 g 175 t
ORIGIN

Query Match 67.5%; Score 285.4; DB 10; Length 820;
Best Local Similarity 83.0%; Pred. No. 1.4e-63;
Matches 351; Conservative 0; Mismatches 66; Indels 6; Gaps 2;

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/clone="IMAGE:4765669"
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT      171 a   257 c   221 g   165 t
ORIGIN

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Query Match      67.0%; Score 283.2; DB 10; Length 814;
Best Local Similarity 84.0%; Pred. No. 5.3e-63;
Matches 358; Conservative 0; Mismatches 58; Indels 10; Gaps 3;

QY 1 ATGAACACCTGTGGTCTCTCTCCCTGGTGGGAGCTCCAGATGGTCTGTGCCAG 60
Db 1111111111111111111111111111111111111111111111111111111
24 ATGAACACCTGTGGTCTCTCTCCCTGGTGGGAGCTCCAGATGGTCTGTGCCAG 83
QY 61 CTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 1111111111111111111111111111111111111111111111111111111
84 CTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 143
QY 121 TGGCGTGTCTCTGGTGGCTCTCTACAGCTAGTA---ACTGGTGGACCTGGATCCGCCAG 177
Db 1111111111111111111111111111111111111111111111111111111
144 TGCAGTGTCTCTGGTGGCTCCATCAGCAGTAGTAGTATTACTGGGGTGGATCCGCCAG 203
QY 178 CCCCCAGGAGGAGCTGGAGTGGATTTGGACATCTCTCTGGTAGTGGTGGGCCACCAAC 237
Db 1111111111111111111111111111111111111111111111111111111
204 TCCCCAGGAGGAGCTGGAGTGGATTTGGAGTATCTATTATA---GTGGGAACACCTAC 260
QY 238 TACAACCCGTCCTCAAGAGTGCAGTATCATTTTACAAGACAGCTCCAGAACAGATTC 297
Db 1111111111111111111111111111111111111111111111111111111
261 TACAACCCGTCCTCAAGAGTGCAGTATCATTTTACAAGACAGCTCCAGAACAGATTC 320
QY 298 TCCTTGAACCTGAACCTCTGTGACCCGCGGACAGCGCGTGTATTACTGTGCCAGAT 357
Db 1111111111111111111111111111111111111111111111111111111
321 TCCTTGAACCTGAACCTCTGTGACCCGCGGACAGACAGCGTGTATTACTGTCCGAGAT 380
QY 358 TGGGCCCCAATAAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTACCCGTC 417
Db 1111111111111111111111111111111111111111111111111111111
381 GTTGGCTACAGCTTTGGTGAA---TGTGACTACTGGGGCCAGGAACCTGTGTACCCGTC 436
QY 418 TCCTCA 423
Db 437 TCCTCA 442

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RESULT 11
BG685592      736 bp   mRNA   linear   EST 01-MAY-2001
LOCUS        602637569F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4765168 5',
DEFINITION   mRNA sequence.
ACCESSION    BG685592
VERSION      BG685592.1 GI:13916989
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 736)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
CONTACT      Contact: Robert Strausberg, Ph.D.
COMMENT      Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

```

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LLC1623 row: j column: 17  
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#### FEATURES

Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:4765168"  
 /clone\_lib="NIH\_MGC\_48"  
 /tissue\_type="primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
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 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

BASE COUNT 156 a 242 c 200 g 138 t

#### ORIGIN

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Query Match      66.4%; Score 281; DB 10; Length 736;
Best Local Similarity 85.6%; Pred. No. 1.9e-62;
Matches 364; Conservative 0; Mismatches 45; Indels 16; Gaps 4;

QY 1 ATGAACACCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
Db 1111111111111111111111111111111111111111111111111111111
28 ATGAACACCTGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 87
QY 61 CTGCAGCTGCAGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 1111111111111111111111111111111111111111111111111111111
88 GTGCAGCTGCAAGAGTCCGGCCAGGAGTGGTGAAGCCTTCGGAGACCTGTCCCTCACC 147
QY 121 TGGCGTGTCTCTGGTGGCTCTCTCAGCAGTAGTA---ACTGGTGGACCTGGATCCGCCAG 180
Db 1111111111111111111111111111111111111111111111111111111
148 TGCAGTGTCTCTGGTGGCTC---CATCAGTAGTACTACTGTGGAGCTGGATCCGCCAG 204
QY 181 CCAGGAGGAGGAGCTGGAGTGGATTTGGACATCTCTGTGTAGTGGTGGGCCACCACTAC 240
Db 1111111111111111111111111111111111111111111111111111111
205 GCAGGAGGAGGAGCTGGAGTGGATTTGGATATCTCTCACA---GTGGGAGCACCACCTAC 261
QY 241 AACCCGTCCTCAAGAGTGCAGTGCATCATTTTACAAGACAGCTCCAGAACAGATTCCTC 300
Db 1111111111111111111111111111111111111111111111111111111
262 AACCCGTCCTCAAGAGTGCAGTGCATCATTTTACAAGACAGCTCCAGAACAGATTCCTC 321
QY 301 CTGAACCTGAACCTGTGACCCGCGGACAGCGCGTGTATTACTGTGCCAGATTTGG 360
Db 1111111111111111111111111111111111111111111111111111111
322 CTGAGACTGAACCTGTGACCCGCGGACAGCGCGTGTATTACTGTGCCAGATG----- 376
QY 361 GCCCAANTAGCTGGAACAAACGC--TAGGCTTCTGGGGCCAGGAGTCTCTGTGACCGTCT 418
Db 1111111111111111111111111111111111111111111111111111111
377 ---GCAGCAGCTGGGAGCTTCGCTTTTGACTACTTGGGGCCAGGAAACCTCTGTACCGTCT 433
QY 419 CCTCA 423
Db 434 CCTCA 438

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#### RESULT 12

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BM008069
LOCUS        603617839F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5451057 5',
DEFINITION   mRNA sequence.
ACCESSION    BM008069
VERSION      BM008069.1 GI:16522423

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Db	394	GAGACCCTTAATAGTGGGACCTACAGTAAGTTTGACCACTGGGGCCAGGGAACCTGGTC	453
Qy	412	ACCGTCTCCTCA	423
Db	454	ACCGTCTCCTCA	465
RESULT	14		
BG548421			
LOCUS	602575006F1	NIH_MGC_77	729 bp mRNA linear EST 04-APR-2001
DEFINITION	729 bp mRNA linear EST 04-APR-2001		
ACCESSION	BG548421		
VERSION	1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 729)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-f@mail.nih.gov		
	Tissue Procurement: CLONTECH Laboratories, Inc.		
	cDNA Library Preparation: CLONTECH Laboratories, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Plate: L1CMI541 row: k column: 01		
	High quality sequence stop: 711.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:4703352"		
	/clone_lib="NIH_MGC_77"		
	/lab_host="DH10B (T1 phage-resistant)"		
	Note="Organ: lung; Vector: pDNK-LfB (Clontech); Site:1: SfiI (ggcgctctgcgc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGGCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
BASE COUNT	141 a	238 c	208 g 142 t
ORIGIN			
Query Match	66.2%	Score 280;	DB 10; Length 729;
Best Local Similarity	85.2%	Pred. No. 3.4e-62;	
Matches 363;	Conservative	0; Mismatches	50; Indels 13; Gaps 4;
Qy	1	ATGAACACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCCGAG	60
Db	36	ATGAAGCACCTGTGGTTCTTCTCTCTGTGGCAGCTCCAGATGGGTCTGTCCCGAG	95
Qy	61	CTGCAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCACC	120
Db	96	CTGCAGCTGCAGGAGTCCGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCTACCTACC	155
Qy	121	TGCCTGTCTCTGTGGCTCTGTGCAGCAGTAGTA--ACTGGTGACCTGGATCGGCCAG	177
Db	156	TGCATTGTCTCTGTGGTGTTCACACGACGAGTAGTAGTCACTACTGGGGCTGGATCGGCCAG	215
Qy	178	CCCCCAGGGAAGGACTGGAGTGGATTGGAGCGTATCTCTGGTAGTGGTGGGGCCACCAAC	237

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Db 51 ATGAACACCTGTGGTTCTTCTCTCTCTGGTGGCAGCTCCAGATGGTCTGTCCAG 110
QY 61 CTGCAGCTGCAGAGTGGGGCCAGAGTGTGAAGCCTTCGGAGACCTGTCCCTCACC 120
Db 111 GTGCAGCTACACAGTGGGGCCAGAGCTGTGAAGCCTTCGGAGACCTGTCCCTCACC 170
QY 121 TCGGTGTCTCTGGTGGTCTCTCAGCAGTAGTAAGTGGTGGACCTGGATCGCCAGCCC 180
Db 171 TCGGTGTCTATGGTGGTCTCTCAGCAGTAGTAAGTGGTGGACCTGGATCGCCAGCCC 227
QY 181 CCAGGGAAGGACTGGAGTGGATGGACGTATCTCTGGTAGTGGTGGGCCACCAACTAC 240
Db 228 CCAGGGAAGGCTGGAGTGGATGGGAAATCAATCATAGTGAAG--CACCAACTAC 284
QY 241 AACCCGTCCCTCAAGAGTCGAGTCATCTTCAAGACACGTCCAAGAACCAAGTCTCC 300
Db 285 AACCCGTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTCTCC 344
QY 301 CTGAACCTGAAGTGTGACCGCCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
Db 345 CTGAAGCTGAGCTCTGTGACCGCCGGACACGGCTGTATTACTGTGCCAGAGCGAT 404
QY 361 GCCCAATAGCTGGAACACGCTAGGCTCTGGGGCCAGGGAGTCTGTGTACCGCTCTCC 420
Db 405 GGCTACAATTCGATGATGCTTTTGATATCTGGGGCCAGGGACAATGGTCAACCGTCTCT 464
QY 421 TCA 423
Db 465 TCA 467
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Job time: 4510 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:58:36 ; Search time 488.47 Seconds  
(without alignments)  
1486.795 Million cell updates/sec

Title: US-09-019-441-2  
Perfect score: 423  
Sequence: 1 ATGAACACCTGTGGTCTT.....TCTGTGTCACCGTCTCTCA 423

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_032802.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	423	19 AAV33308	Anti-human CD23 6G
2	313.2	74.0	1431	18 AAT62513	Primate anti-hu
3	313.2	74.0	1431	19 AAV35489	Macaque primate
4	313.2	74.0	1431	24 AAS17247	DNA sequence of a
5	301.2	71.2	423	21 AAZ39331	Nucleotide sequenc
6	299.8	70.9	1404	18 AAT62868	Human gamma-4 heav
7	299.8	70.9	1404	18 AAT62869	Human gamma-4E hea
8	299.8	70.9	1404	18 AAT62870	Human gamma-4E he
9	298.2	70.5	420	21 AAZ39335	Nucleotide sequenc

10	298.2	70.5	423	14 AAO35903	Anti-CD4 VH coding
11	298.2	70.5	423	18 AAT91564	Anti-CD4 cynomolgu
12	298.2	70.5	423	19 AAV31428	Anti-CD4 antibody
13	298.2	70.5	423	19 AAV05695	Monkey anti-CD4 he
14	296.4	70.1	619	22 AAS03048	Human diagnostic a
15	295.2	69.8	420	18 AAT95167	Monkey anti-human
16	295.2	69.8	420	18 AAT62865	Monkey anti-CD4 he
17	295.2	69.8	420	19 AAV23760	Anti-CD4 antibody
18	293.8	69.5	496	20 AAZ24416	Human bladder tumo
19	293.4	69.4	417	21 AAA52907	Human LH1238 mono
20	292.4	69.1	1431	18 AAT62510	Primate anti-hu
21	292.4	69.1	1431	19 AAV35485	Macaque primate
22	292.4	69.1	1431	24 AAS17243	DNA sequence of a
23	290	68.6	1634	21 AAZ50012	Human immune syste
24	289.6	68.5	1567	22 AAC66522	Human immune syste
25	287.6	68.0	614	20 AAV86218	EST clone O99. Ho
26	286	67.6	417	21 AAA13938	Human PTHrp monoc
27	281.4	66.5	397	20 AAZ24417	Human bladder tumo
28	276.2	65.3	1746	21 AAZ27382	Human IGFAM-2 immu
29	275.6	65.2	348	14 AAO42697	Vh 71-4. Homo sap
30	275.6	65.2	348	14 AAO42699	VH411. Homo sapie
31	275.6	65.2	348	14 AAO42700	VH415. Homo sapie
32	274	64.8	348	14 AAO42701	VH416. Homo sapie
33	273.6	64.7	457	20 AAZ24423	Human bladder tumo
34	273.4	64.6	1507	21 AAO09695	Human immunoglobul
35	272.8	64.5	1431	17 AAT18059	Monoclonal antibod
36	270	63.8	1543	22 AAF97947	Human secreted pro
37	269.6	63.7	408	18 AAT79919	Immunoglobulin rB6
38	269.6	63.7	426	14 AAO49154	F105 rearranged va
39	269.4	63.7	456	21 AAZ24290	Human 5' EST isola
40	269.4	63.7	1644	20 AAZ24434	Human bladder tumo
41	269.2	63.6	459	21 AAZ42288	Human 5' EST isola
42	267.6	63.3	351	14 AAO42702	AD26. Homo sapien
43	266.6	63.0	393	21 AAC98188	Human colon cancer
44	266.2	62.9	403	18 AAT73440	Human immunoglobul
45	266.2	62.9	403	19 AAV39238	Functional gamma t

#### ALIGNMENTS

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RESULT 1
AAV33308
ID AAV33308 standard; DNA; 423 BP.
XX AC AAV33308;
XX DT 18-NOV-1998 (first entry)
XX DE Anti-human CD23 6G5 monoclonal antibody heavy chain variable region DNA.
XX KW Anti-human CD23 6G5 monoclonal antibody; heavy chain variable region;
KW human CD23; IgE; FcER1/CD23; gamma-1 constant region;
KW gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
XX OS Macaca fascicularis
XX FH Key
XX FT CDS
XX FT Location/Qualifiers
XX FT /*tag= a
XX FT /product= "anti-human CD23 6G5 heavy chain variable
XX FT /note= "CDS does not contain a stop codon"
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XX FT sig_peptide
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XX FT /*tag= c
XX FT misc_feature
XX FT /*tag= d
XX FT /note= "encodes CDR 1 region"
XX FT 208..258
XX FT misc_feature
XX FT /*tag= e

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XX  Hanna N, Newman RA, Reff ME;
PI  WPI: 1997-201913/18.
DR  P-PSDB; AAW14926.
XX
XX  Chimeric antibody comprising monkey variable domains and human
PT  constant domains - affects CD4-mediated immune functions, esp.
PT  useful for treatment of autoimmune disease, e.g. rheumatoid
PT  arthritis
XX
XX  Disclosure: Page 86-88; 155pp; English.
XX
XX  DNA sequences (AAT62868-70) respectively code for the heavy chain
CC  regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC  mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC  mutations. They can be used to provide novel monoclonal and
CC  chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC  gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC  combined with the antigen binding domains (see also AAW14922-23) of
CC  macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC  show high affinity to human CD4, have little or no immunogenicity
CC  in humans and show reduced or absence of effector function. The
CC  gamma-4E and -4PE mutations confer activity enhanced stability and
CC  eliminate depleting activity. The antibodies can be used to treat
CC  autoimmune diseases such as rheumatoid arthritis.
XX
XX  Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;

Query Match      70.9%; Score 299.8; DB 18; Length 1404;
Best Local Similarity 83.5%; Pred. No. 4.5e-68;
Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

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DB  1 atgaacacctgtgttctctctctctctctgtggcagccccagatgggtctgtccag 60

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QY  121 TCGGCTGTCTGTGGTCTCTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTCTCCAG 180
DB  121 tcggctgtctgtggctctctctctctctgtgggagaccttcagatgggtctgtccag 180

QY  121 tgcagtgctctgtgtggtccatcagcgggtgactattattgttctgtggtccagtc 180
DB  121 tgcagtgctctgtgtggtccatcagcgggtgactattattgttctgtggtccagtc 180

QY  181 CCAGGAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 240
DB  181 ccaggagagggagtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 240

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QY  301 CTGAACCTGGAACCTGTGACCCCGGACACAGCCCGGTGATATCTGTGCCAGAGATTGG 360
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DB  358 atattgaataatcttcaactggttattactgtggggccagggagtgctgtgaccgtctcc 417

QY  421 TCA 423
DB  418 tca 420

RESULT
ID AAT62870
XX AAT62870 standard; DNA; 1404 BP.
XX AAT62870;
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DT  18-OCT-1997 (first entry)
XX  Human gamma-4PE heavy chain DNA.
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XX  CD4; monoclonal antibody; chimeric antibody; recombinant antibody;
KW  cynomolgus monkey; autoimmune disease; rheumatoid arthritis;
KW  leukaemia; lymphoma; graft-versus-host disease; asthma;
KW  transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
XX
XX  Homo sapiens.
XX
XX  WO9709351-A1.
XX
XX  13-MAR-1997.
XX
XX  05-SEP-1996; 96WO-US14324.
XX
XX  06-SEP-1995; 95US-0523894.
XX
XX  (IDEC-) IDEC PHARM CORP.
XX
XX  Hanna N, Newman RA, Reff ME;
XX
XX  WPI: 1997-201913/18.
DR  P-PSDB; AAW14927.
XX
XX  Chimeric antibody comprising monkey variable domains and human
PT  constant domains - affects CD4-mediated immune functions, esp.
PT  useful for treatment of autoimmune disease, e.g. rheumatoid
PT  arthritis
XX
XX  Disclosure: Page 91-93; 155pp; English.
XX
XX  DNA sequences (AAT62868-70) respectively code for the heavy chain
CC  regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E
CC  mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P
CC  mutations. They can be used to provide novel monoclonal and
CC  chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9
CC  gamma-4PE, in which the human IgG4 Fc binding domain framework is
CC  combined with the antigen binding domains (see also AAW14922-23) of
CC  macaque anti-human CD4 monoclonal antibody E9.1. These antibodies
CC  show high affinity to human CD4, have little or no immunogenicity
CC  in humans and show reduced or absence of effector function. The
CC  gamma-4E and -4PE mutations confer activity enhanced stability and
CC  eliminate depleting activity. The antibodies can be used to treat
CC  autoimmune diseases such as rheumatoid arthritis.
XX
XX  Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;

Query Match      70.9%; Score 299.8; DB 18; Length 1404;
Best Local Similarity 83.5%; Pred. No. 4.5e-68;
Matches 353; Conservative 0; Mismatches 67; Indels 3; Gaps 1;

QY  1 ATGAACACCTGTGTTCTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTCTCCAG 60
DB  1 atgaacacctgtgttctctctctctctctgtggcagccccagatgggtctgtccag 60

QY  61 CTCGAGCTCGAGAGTCGGGGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCTCCAC 120
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QY  121 TCGGCTGTCTGTGGTCTCTCTCTCTCTGTGGGAGCTCCAGATGGTCTGTCTCCAG 180
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QY  181 CCAGGAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 240
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DB  241 aatccctccctcaaatcgatgctccatttcaatagacacgtccaaagaacctctctcc 300

QY  301 CTGAACCTGGAACCTGTGACCCCGGACACAGCCCGGTGATATCTGTGCCAGAGATTGG 360
DB  301 ctgaacctggaacctgtgaccccgacacagcccggtgatattctgtgctgagtaatt 360

QY  361 GCCCAATAGCTGGAACACACGTAGCTTCTGGGGCCAGGGAGTCTGTGACCCGTC 420
DB  358 atattgaataatcttcaactggttattactgtggggccagggagtgctgtgaccgtctcc 417

QY  421 TCA 423
DB  418 tca 420

RESULT
ID AAT62870
XX AAT62870 standard; DNA; 1404 BP.
XX AAT62870;
XX

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Db 304 ctgaaactgaggtctgtgacccgctgacacgctctattactgtgcgagtaat--- 360  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	100.0	423	423	16	US-09-292-053-3
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4	313.2	74.0	1431	17	US-09-383-916-11
5	313.2	74.0	1431	22	US-09-576-424-11
6	304.4	72.0	681	26	US-09-665-486-420
7	304.4	72.0	681	55	US-60-168-599-709
8	303.2	71.7	541	31	US-09-824-559-7148
9	301.2	71.2	423	1	PCT-US99-09131-40
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35 291.6 68.9 1540 28 US-09-710-281-5770 Sequence 5770, Ap  
36 291.6 68.9 1540 29 US-09-726-172-1935 Sequence 1935, Ap  
37 290.8 68.7 1431 11 US-08-746-361-2 Sequence 2, Appli  
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39 290.2 68.6 600 26 US-09-665-486-418 Sequence 418, App  
40 290.2 68.6 600 55 US-60-168-599-708 Sequence 708, App  
41 290 68.6 1605 16 US-09-205-070-16228 Sequence 16228, A  
42 290 68.6 1605 17 US-09-340-623-16228 Sequence 16228, A  
43 290 68.6 1605 33 US-09-898-888-16228 Sequence 16228, A  
44 290 68.6 1605 33 US-09-898-888A-16228 Sequence 16228, A  
45 290 68.6 1634 15 US-09-107-223A-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-019-441-2  
; Sequence 2, Application US/09019441  
; GENERAL INFORMATION:  
; APPLICANT: REFF, Mitchell E.  
; KLOETZER, William S.  
; NAKAMURA, Takehiko  
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/019,441  
; FILING DATE: 05-Feb-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/803,085  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-502  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..423  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 58..423  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-019-441-2

Query Match , 100.0%; Score 423; DB 14; Length 423;

Best Local Similarity 100.0%; Pred. No. 1.3e-96;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 ATGAACACCTGTGGTTCCTCTCCCTCCCTGGTGGAGAGCTCCAGAGTGGTCTGTGCTCCAG 60  
QY 61 CTGCAGCTCAGAGAGTCGGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCACC 120  
DB 61 CTGCAGCTCAGAGAGTCGGGGCCAGGAGTGGTGAAGCCCTTCGGAGACCCCTGTCCCTCACC 120  
QY 121 TCGCGTGTCTCTGGTGGCTCTGTGTACAGTAGTAACTGTGTGGACCTGTGGATCCGCCAGCCC 180  
DB 121 TCGCGTGTCTCTGGTGGCTCTGTGTACAGTAGTAACTGTGTGGACCTGTGGATCCGCCAGCCC 180  
QY 181 CCAGGGAAGGAGTGGAGTGGATTTGACCTATCTCTGGTAGTGGTGGGGCCCAACTAC 240  
DB 181 CCAGGGAAGGAGTGGAGTGGATTTGACCTATCTCTGGTAGTGGTGGGGCCCAACTAC 240  
QY 241 AACCCGTCCTCAAGAGTCGAGTCATCATTTACAAAGACACAGCTCCAAAGAACCAAGTTCTCC 300  
DB 241 AACCCGTCCTCAAGAGTCGAGTCATCATTTACAAAGACACAGCTCCAAAGAACCAAGTTCTCC 300  
QY 301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCGAGAGATTGG 360  
DB 301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGGCGGTGTATTACTGTGCGAGAGATTGG 360  
QY 361 GCCCAATAAGCTGGGAACAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCC 420  
DB 361 GCCCAATAAGCTGGGAACAACGCTAGGCTTCTGGGGCCAGGAGTCTCTGGTCAACCGTCTCC 420  
QY 421 TCA 423  
DB 421 TCA 423

RESULT 2

US-09-292-053-3  
; Sequence 3, Application US/09292053  
; GENERAL INFORMATION:  
; APPLICANT: REFF, MITCHELL E.  
; APPLICANT: KLOETZER, WILLIAM S.  
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE  
; FILE REFERENCE: 23522.0699  
; CURRENT APPLICATION NUMBER: US/09/292,053  
; CURRENT FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: 08/803,085  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 423  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: (1)..(58)  
; NAME/KEY: mat\_peptide  
; LOCATION: (58)..(423)  
; NAME/KEY: CDS  
; LOCATION: (1)..(423)  
US-09-292-053-3

Query Match  
Best Local Similarity 100.0%; Score 423; DB 16; Length 423;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 atgaacacctgtggttct 60



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Db	61	ctgacgtcgaggagtcgggcccaggagtggtgaagccttcggagaccctgtccctcacc	120
QY	121	TGGCGTCTCTGGTGGCTCTGTACAGCAGTAGTAACCTGGTGGACCTGGATCGCGCAGGCC	180
Db	121	tgcgtgtctctggtgctctgtcgagcagtagtaactggtggaacctggatccgcgacgcc	180
QY	181	CCAGGGAAGGGACTGCAGTGGATTGGACGTATCTGTGTAGTGGTGGGCCACCAACTAC	240
Db	181	ccagggaaggacgtggattggacgtactctctggtagttggtgggcccaccactac	240
QY	241	AACCCGTCCCTCAAGAGTCGAGTCATCTTTCACAAGACACCTCCAAGAACACAGTTCTCC	300
Db	241	aaccccctcctaagtgtcgagtcacacttcacaagacacgtcccaagaacacagttctctcc	300
QY	301	CTGAACCTGAACCTCTGTGACCCGCCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG	360
Db	301	ctgaacctgaactctgtgaccgccgcgacacggtccgtgtattactgtgtccagaagattgg	360
QY	361	GCCCAATAGCTGGAAACACGCTAGGCTTCTGGGGCCAGGGAGTCCTGTGTACCCGTCC	420
Db	361	gcccaaatagctggaacaacgtagcttctgggcccaggagtcctgtgtaccctgtctcc	420
QY	421	TCA 423	
Db	421	tca 423	

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RESULT      3
US-08-746-361-6
; Sequence 6, Application US/08746361
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; APPLICANT: HANNA, Nabil
; APPLICANT: BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; TITLE OF INVENTION: INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
; TITLE OF INVENTION: AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,361
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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RESULT 4  
US-09-383-916-11  
; Sequence 11, Application US/09383916  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/383.916  
; FILING DATE: 26-AUG-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/487,550  
; FILING DATE: 07-JUN-1995

RESULT 6  
US-09-665-486-420  
; Sequence 420, Application US/09665486  
; GENERAL INFORMATION:  
; APPLICANT: Hodgson, David M.  
; APPLICANT: Lincoln, Stephen E.  
; APPLICANT: Russo, Frank D.  
; APPLICANT: Spiro, Peter A.  
; APPLICANT: Banville, Steve C.  
; APPLICANT: Bratcher, Shawn R.  
; APPLICANT: Dufour, Gerard E.  
; APPLICANT: Cohen, Howard J.  
; APPLICANT: Rosen, Bruce H.  
; APPLICANT: Shah, Purvi  
; APPLICANT: Chalup, Michael S.  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Jones, Anissa L.









GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
APPLICANT: Newman, Roland A.  
APPLICANT: Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
TITLE OF INVENTION: Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/612,914  
FILING DATE: 10-JUL-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/523,894  
FILING DATE: 06-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1404 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1404  
NAME/KEY: mat\_peptide  
LOCATION: 1..1404  
US-09-612-914-11

Query Match 70.9%; Score 299.8; DB 23; Length 1404;  
Best Local Similarity 83.5%; Pred. No. 2.2e-65;  
Matches 553; Conservative 0; Mismatches 67; Indels 3; Gaps 1;  
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DB 1 ATGAACACCTGTGGTCTCTCCCTGCTGGGAGCTCCAGATGGGTCTGTCCTCCAG 60  
QY 61 CTGCAGCTCAGAGTCGGGGCCAGAGTGGTGAAGCTTCGGAGACCTGCTCCCTCACC 120  
DB 61 GTGCAGCTCAGAGTCGGGGCCAGAGTGGTGAAGCTTCGGAGACCTGCTCCCTCACC 120  
QY 121 TCGCTGTCTCTGGTGGCTCTCTCAGCAGTACTAGTGGTGGACCTGGATCGCCAGCC 180  
DB 121 TCGAGTGTCTCTGGTGGCTCTCTCAGCAGTACTAGTGGTGGATCGCCAGCTCC 180  
QY 181 CCAGGAAGGAGTGGAGTGGATGGACCTATCTGTGTAGTGGTGGGCGCCACCACTAC 240  
DB 181 CCAGGAAGGAGTGGAGTGGATGGACCTATCTGTGTAGTGGTGGGCGCCACCACTAC 240

QY 241 AACCCGTCCTCAAGAGTCGAGTCATCATTTTCAAGACACGCTCCAAAGAACAGTTCTCC 300  
DB 241 AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACAGCTCCAAAGAACCTCTTCTCC 300  
QY 301 CTGAACCTGAACCTCTGTGACCCCGGACGACGGCGGTGTTACTGTGCCAGAGTTGG 360  
DB 301 CTGAACCTGAACCTCTGTGACCCCGGACGACGGCGGTGTTACTGTGCCAGAGTTGG 360  
QY 361 GCCCAATAGCTGGAACAACGCTAGGCTTCTGGGCGCCAGGAGTCTGTGTCACCGTCTCC 420  
DB 361 GCCCAATAGCTGGAACAACGCTAGGCTTCTGGGCGCCAGGAGTCTGTGTCACCGTCTCC 420  
QY 421 TCA 423  
DB 421 TCA 420  
RESULT 15  
US-09-612-914A-7  
Sequence 7, Application US/09612914A  
GENERAL INFORMATION:  
APPLICANT: Hanna, Nabil  
Newman, Roland A.  
Reff, Mitchell E.  
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human  
Therapy  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314-3187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/612,914A  
FILING DATE: 10-Jul-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/523,894  
FILING DATE: 06-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1404 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: heavy chain variable and constant gamma 4  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1404  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..1404  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-612-914A-7





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:58:38 ; Search time 662.78 Seconds  
(without alignments)  
2056.838 Million cell updates/sec

Title: US-09-019-441-2  
Perfect score: 423  
Sequence: 1 ATGAACACCTGGTCTT.....TCTGGTCACCGTCTCTCA 423

Scoring table:  
Gapop 10.0 , Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New.\*

- 1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pna/US05\_NEW\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	423	7	US-10-103-686-2
2	313.2	74.0	1431	5	US-09-758-173-11
3	313.2	74.0	1431	5	US-09-526-098-11
4	313.2	74.0	1431	5	US-09-948-429B-11
5	313.2	74.0	1431	5	US-09-971-631-11
6	313.2	74.0	1431	6	US-10-073-138-6
7	313.2	74.0	1431	7	US-10-124-807-11
8	313.2	74.0	1431	7	US-10-124-905-11
9	313.2	74.0	1431	7	US-10-030-390-11
10	299.8	70.9	1404	6	US-10-211-357-7
11	299.8	70.9	1404	6	US-10-211-357-9
12	299.8	70.9	1404	6	US-10-211-357-11
13	298.2	70.5	423	5	US-09-850-165-15
14	296.4	70.1	619	7	US-10-089-128-37
15	295.2	69.8	420	6	US-10-211-357-1
16	292.4	69.1	1431	5	US-09-758-173-3
17	292.4	69.1	1431	5	US-09-526-098-3
18	292.4	69.1	1431	5	US-09-948-429B-3
19	292.4	69.1	1431	5	US-09-971-631-3
20	292.4	69.1	1431	7	US-10-124-807-3
21	292.4	69.1	1431	7	US-10-124-905-3
22	292.4	69.1	1431	7	US-10-030-390-3
23	290.8	68.7	1431	6	US-10-073-138-2
24	290.4	68.7	798	7	US-10-175-525-164
25	285.4	67.5	1610	6	US-10-206-008-190

26	280	66.2	1022	6	US-10-206-008-348	Sequence 348, App
27	280	66.2	1022	6	US-10-211-364-501	Sequence 501, App
28	277.4	65.6	1407	7	US-10-175-525-162	Sequence 162, App
29	276.2	65.3	1746	5	US-09-831-805A-21	Sequence 21, Appl
30	268.6	63.5	413	5	US-09-918-995-16699	Sequence 16699, A
31	266.2	62.9	1509	7	US-10-175-525-163	Sequence 163, App
32	263.6	62.3	1584	5	US-09-831-805A-35	Sequence 35, Appl
33	262.6	62.1	1641	6	US-10-208-008-125	Sequence 125, App
34	257.4	60.9	450	5	US-09-582-337-13	Sequence 13, Appl
35	254.2	60.1	438	5	US-09-918-995-16650	Sequence 16650, A
36	251.8	59.5	414	1	PCT-US02-16087-4	Sequence 4, Appli
37	251.8	59.5	414	7	US-10-153-437-4	Sequence 4, Appli
38	248.6	58.8	1648	6	US-10-206-008-124	Sequence 124, App
39	248	58.6	2244	6	US-10-198-846-13582	Sequence 13582, A
40	247	58.4	421	5	US-09-547-599C-620	Sequence 620, App
41	243.2	57.5	1092	6	US-10-206-008-21	Sequence 21, Appl
42	243	57.4	3128	7	US-10-027-632-114467	Sequence 114467, A
43	239	56.5	505	1	PCT-US02-25766-6460	Sequence 6460, Ap
44	236.2	55.8	362	6	US-10-203-135-20932	Sequence 20932, A
45	234.8	55.5	319	6	US-10-182-993-20398	Sequence 20398, A

## ALIGNMENTS

RESULT 1  
US-10-103-686-2  
; Sequence 2, Application US/10103686  
; GENERAL INFORMATION:  
; APPLICANT: REFF, Mitchell E.  
; KLOETZER, William S.  
; NAKAMURA, Takehiko  
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; City: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/103,686  
; FILING DATE: 25-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/803,085  
; FILING DATE: 20-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-353  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 423 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..423  
; FEATURE:  
; NAME/KEY: mat\_peptide

LOCATION: 58...423  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-10-103-686-2

Query Match 100.0%; Score 423; DB 7; Length 423;  
Best Local Similarity 100.0%; Pred. No. 4.3e-97;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGAGCTCCAGATGGTCTGTCCCAAG 60  
DB 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGAGCTCCAGATGGTCTGTCCCAAG 60  
QY 61 CTGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120  
DB 61 CTGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120  
QY 121 TGGCTGTCTGTGGTCTGTGACAGTAGTAAGTGTGACCTGTGGATCGCCAGCCC 180  
DB 121 TGGCTGTCTGTGGTCTGTGACAGTAGTAAGTGTGACCTGTGGATCGCCAGCCC 180  
QY 181 CCAGGAAGGAGTGGAGTGGATGGACCTATCTCTGTAGTGGTGGGCCCACTAC 240  
DB 181 CCAGGAAGGAGTGGAGTGGATGGACCTATCTCTGTAGTGGTGGGCCCACTAC 240  
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DB 241 AACCCCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACGTCCTCAAGAACAGTTCTCC 300  
QY 301 CTGAACCTGAACCTGTGACCGCGGGACAGCGCGTGTATTACTGTCCAGAGATTGG 360  
DB 301 CTGAACCTGAACCTGTGACCGCGGGACAGCGCGTGTATTACTGTCCAGAGATTGG 360  
QY 361 GCCCAATAGCTGGAACACGCTAGCTTCTGGGGCCAGGAGTCTGTGACCGTCTCC 420  
DB 361 GCCCAATAGCTGGAACACGCTAGCTTCTGGGGCCAGGAGTCTGTGACCGTCTCC 420  
QY 421 TCA 423  
DB 421 TCA 423

RESULT 2

US-09-758-173-11  
Sequence 11, Application US/09758173  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/758,173  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/383,916  
FILING DATE:  
APPLICATION NUMBER: US 08/487,550  
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-131  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1431 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1431  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 1..1431  
US-09-758-173-11

Query Match 74.0%; Score 313.2; DB 5; Length 1431;  
Best Local Similarity 84.5%; Pred. No. 2.1e-69;  
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGAGCTCCAGATGGTCTGTCCCAAG 60  
DB 1 ATGAACACCTGTGGTCTCTCCCTCCCTGGTGGAGCTCCAGATGGTCTGTCCCAAG 60  
QY 61 CTGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120  
DB 61 CTGACCTGCAGAGTCGCGGCCAGGAGTGGTGAAGCTTCGAGACCTGTCCCTCACC 120  
QY 121 TGGCTGTCTGTGGTCTGTGACAGTAGTAAGTGTGACCTGTGGATCGCCAGCCC 180  
DB 121 TGGCTGTCTGTGGTCTGTGACAGTAGTAAGTGTGACCTGTGGATCGCCAGCCC 180  
QY 181 CCAGGAAGGAGTGGAGTGGATGGACCTATCTCTGTAGTGGTGGGCCCACTAC 240  
DB 181 CCAGGAAGGAGTGGAGTGGATGGACCTATCTCTGTAGTGGTGGGCCCACTAC 240  
QY 241 AACCCCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACGTCCTCAAGAACAGTTCTCC 300  
DB 241 AACCCCTCCCTCAAGAGTCGAGTCATCATTTCAAGACACGTCCTCAAGAACAGTTCTCC 300  
QY 301 CTGAACCTGAACCTGTGACCGCGGGACAGCGCGTGTATTACTGTCCAGAGATTGG 360  
DB 301 CTGAACCTGAACCTGTGACCGCGGGACAGCGCGTGTATTACTGTCCAGAGATTGG 360  
QY 361 GCCCAATAGCTGGAACAA-----CGTAGGCTTCTGGGGCCAGGAGTCT 405  
DB 361 CTTTTCAGTGTGGAATGTTTACAACTGTTTCGATGTCTGTGGGCCGGGAGTC 420  
QY 406 CTGTCACCGTCTCTCTCA 423  
DB 421 CTGTCACCGTCTCTCTCA 438

RESULT 3

US-09-526-098-11  
Sequence 11, Application US/09526098  
GENERAL INFORMATION:  
APPLICANT: Anderson, Darrell R.  
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince Street





```
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-073-138-6

Query Match 74.0%; Score 313.2; DB 6; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.1e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAACACCTGTGGTTCCTCTCCCTGCTGGGAGAGTCCAGAGTGGTGGTCCAG 60
DB 1 ATGAACACCTGTGGTTCCTCTCCCTGCTGGGAGAGTCCAGAGTGGTGGTCCAG 60
QY 61 CTGCAGCTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC 120
DB 61 GTGCAGCTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC 120
QY 121 TGGCTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGTGGACCTGCGCCAGAGCC 180
DB 121 TGGCTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGTGGACCTGCGCCAGAGCC 180
QY 181 CCAGGGAAGGAGCTGGAGTGGATTTGACATCTCTCTGGTGGGAGGCGCCAGAGTAC 240
DB 181 CCAGGGAAGGAGCTGGAGTGGATTTGACATCTCTCTGGTGGGAGGCGCCAGAGTAC 240
QY 241 AACCCGTCCTCAAGAGTCGAGTCATCTTACACAGACAGCTCCCAAGACAGTTCCTCC 300
DB 241 AACCCGTCCTCAAGAGTCGAGTCATCTTACACAGACAGCTCCCAAGACAGTTCCTCC 300
QY 301 CTGAACCTGAACCTCTGTACCGCGGAGACAGCGCGTGTATTACTGTGCGAGAGATTGG 360
DB 301 CTGAACCTGAACCTCTGTACCGCGGAGACAGCGCGTGTATTACTGTGCGAGAGATTGG 360
QY 361 GCCCAATAGCTGGAACAA-----CGCTAGGCTTCTGGGCGCCAGGAGTC 405
DB 361 CTTTTTTCAGTTGTTGAATGTTTACAAACAGTGGTTCGATGCTCTGGGCGCGGAGTC 420
QY 406 CTGGTCACCGTCTCCTCA 423
DB 421 CTGGTCACCGTCTCCTCA 438

RESULT 7
US-10-124-807-11
; Sequence 11, Application US/10124807
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
```

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; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,807
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
; US-10-124-807-11
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Query Match 74.0%; Score 313.2; DB 7; Length 1431;
Best Local Similarity 84.5%; Pred. No. 2.1e-69;
Matches 370; Conservative 0; Mismatches 53; Indels 15; Gaps 1;

QY 1 ATGAACACCTGTGGTTCCTCTCCCTGCTGGGAGAGTCCAGAGTGGTGGTCCAG 60
DB 1 ATGAACACCTGTGGTTCCTCTCCCTGCTGGGAGAGTCCAGAGTGGTGGTCCAG 60
QY 61 CTGCAGCTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC 120
DB 61 GTGCAGCTGCAGGAGTCGGGCGCCAGAGTGGTGAAGCCTTCGGAGACCTGTCCTCACC 120
QY 121 TGGCTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGTGGACCTGCGCCAGAGCC 180
DB 121 TGGCTGTCTCTGGTGGCTCTGTACAGCTAGTAACTGTGGACCTGCGCCAGAGCC 180
QY 181 CCAGGGAAGGAGCTGGAGTGGATTTGACATCTCTCTGGTGGGAGGCGCCAGAGTAC 240
DB 181 CCAGGGAAGGAGCTGGAGTGGATTTGACATCTCTCTGGTGGGAGGCGCCAGAGTAC 240
QY 241 AACCCGTCCTCAAGAGTCGAGTCATCTTACACAGACAGCTCCCAAGACAGTTCCTCC 300
DB 241 AACCCGTCCTCAAGAGTCGAGTCATCTTACACAGACAGCTCCCAAGACAGTTCCTCC 300
QY 301 CTGAACCTGAACCTCTGTACCGCGGAGACAGCGCGTGTATTACTGTGCGAGAGATTGG 360
DB 301 CTGAACCTGAACCTCTGTACCGCGGAGACAGCGCGTGTATTACTGTGCGAGAGATTGG 360
QY 361 GCCCAATAGCTGGAACAA-----CGCTAGGCTTCTGGGCGCCAGGAGTC 405
DB 361 CTTTTTTCAGTTGTTGAATGTTTACAAACAGTGGTTCGATGCTCTGGGCGCGGAGTC 420
QY 406 CTGGTCACCGTCTCCTCA 423
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Query Match 70.5%; Score 298.2; DB 5; Length 423;  
Best Local Similarity 83.2%; Pred. No. 1,1e-65;  
Matches 352; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

OY 1 ATGAAACACCCTGTGGTTCTTCCCTCCTCGTGAGTCAGCTCCCAAGTGGTCTGTGCCAG 60  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
4 atgaaacacctgtgtcttcctcctccctgttggcagccccagatvgtttgtcccag 63

OY 61 CTGCAGCTGCAGAGAGTGCGGGCCCCAGAGTGGTGAACCTTCGGAGACCCTGTCCCTCAC 120  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
64 gtgcagctgcagagagcggygccagagactgtgaagccttcgagaccctgtccctaac 123

OY 121 TGGCCTGTCTCTGTGGTGGCTCTGTGCAGTAGTAAGTAAGTGAGAGCATGGATCCGACCCC 180  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
124 tgcagtgctctctgtgtgtcttcatacagcggtagcatattatgtgtcttgcacgcagctc 183

OY 181 CCAGGAGAAGGAGCTAGAGTGATTGGACGATCTCTGTGTAGTGTTGGGGCCACCACAATAC 240  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
184 ccagaggagaagagcagtggatcgtctacatctatgcaagtgtggtgggagccaattaac 243

OY 241 AACCCGTCCCTCAGAGTGCAGTATCATTTTCAACAAGACAGTCCAGAACATTTCTCC 300  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
244 aaatccctccccaacaatcgagctcattcctaataagacgctcaagaacccctctcc 303

OY 301 CTGAACCTGAACCTGTGTACCGCCGCGGACACGSCCGTGTATCTGTGCAGAGATTGG 360  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
304 ctgaactcgtgagctgtgtgacccgcgcgagaccgcgcgtctatactctgtgagagtaac--- 360

OY 361 GCCCAATAGCTGAGACACGCTAGGCTTCTGGGGCCAGGAGTCTGTGTCACCGTCTCC 420  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
361 atatggaatatcttcacactgttatatactatctggtggcagggagctcgtcacgcgtcc 420

OY 421 TCA 423  
Db | | |  
421 tca 423

RESULT 14  
US-10-089-128-37  
Sequence 37, Application US/10089128  
GENERAL INFORMATION:  
APPLICANT: INCYTE GENOMICS, INC.  
APPLICANT: HODGSON, David M.  
APPLICANT: LINCOLN, Stephen E.  
APPLICANT: RUSSO, Frank D.  
APPLICANT: SPIRO, Peter A.  
APPLICANT: BANVILLE, Steve C.  
APPLICANT: BRATCHER, Shawn R.  
APPLICANT: DUFOUR, Gerard E.  
APPLICANT: COHEN, Howard J.  
APPLICANT: ROSEN, Bruce H.  
APPLICANT: SHAH, Purvi  
APPLICANT: CHALUP, Michael S.  
APPLICANT: HILLMAN, Jennifer L.  
APPLICANT: JONES, Anissa L.  
APPLICANT: YU, Jimmy Y.  
APPLICANT: GREENMALT, Lila B.  
APPLICANT: PANZER, Scott R.  
APPLICANT: ROSEBERRY, Ann M.  
APPLICANT: WRIGHT, Rachel J.  
APPLICANT: CHEN, Wensheng  
APPLICANT: LIU, Tommy F.  
APPLICANT: VAP, Pierre E.  
APPLICANT: STOCKREHER, Theresa K.  
APPLICANT: AMSHEY, Stefan  
APPLICANT: FONG, Willy T.  
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: PT-1066 PCT  
CURRENT APPLICATION NUMBER: US/10/089,128  
CURRENT FILING DATE: 2002-03-22  
PRIORITY APPLICATION NUMBERS: 60/156,294; 60/155,760; 60/155,939; 60/156,565; 60/156,635; 60/167,542; 60/167,522; 60/167,453; 60/167,517;



Db 361 ATATTGAAATATCTTCACCTGCTTATTATCTGCGCCAGGAGACTCCTGCTCACCGTCTCC 420

Search completed: September 23, 2002, 19:58:47  
Job time: 7177 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 18:00:46 ; Search time 110.65 Seconds  
(without alignments)  
939.024 Million cell updates/sec

Title: US-09-019-441-2

Perfect score: 423  
Sequence: 1 ATGAACACCTGTGTTCTT.....TCTGTGACCGTCTCTCA 423

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.NA.\*  
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2.6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2.6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2.6/ptodata/1/ina/PCUTS.COMB.seq:\*  
6: /cgn2.6/ptodata/1/ina/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	423	3	US-08-803-085-2
2	313.2	74.0	1431	3	US-08-487-550-11
3	299.8	70.9	1404	3	US-08-523-894-7
4	299.8	70.9	1404	3	US-08-523-894-9
5	299.8	70.9	1404	3	US-08-523-894-11
6	298.2	70.5	423	1	US-08-379-072A-19
7	298.2	70.5	423	1	US-08-481-869-19
8	298.2	70.5	423	1	US-08-476-237-15
9	295.2	69.8	420	1	US-08-478-039-107
10	295.2	69.8	420	1	US-08-476-349A-107
11	295.2	69.8	420	3	US-08-523-894-1
12	292.4	69.1	1431	3	US-08-487-550-3
13	289.6	68.5	1567	3	US-09-049-672A-17
14	268	63.4	426	2	US-08-480-774A-1
15	266.2	62.9	403	4	US-09-042-353-357
16	266.2	62.9	403	4	US-08-758-417A-205
17	263.8	62.4	404	4	US-09-042-353-355
18	263.8	62.4	404	4	US-08-758-417A-203
19	257.8	60.9	524	4	US-09-042-353-419
20	257.8	60.9	524	4	US-08-758-417A-219
21	257.8	60.9	4926	4	US-09-042-353-418
22	257.8	60.9	4926	4	US-08-758-417A-268
23	257.6	60.9	413	4	US-09-042-353-351
24	257.6	60.9	413	4	US-08-758-417A-199
25	249.4	59.0	624	3	US-08-545-809A-28
26	247	58.4	402	1	US-08-259-372A-5
27	247	58.4	402	1	US-08-468-671-5

28	243	57.4	800	3	US-08-545-809A-55	Sequence 55, Appl
29	241.4	57.1	840	4	US-09-260-527-4	Sequence 4, Appl
30	239.6	56.6	1212	3	US-08-545-809A-61	Sequence 61, Appl
31	238.2	56.3	650	3	US-08-545-809A-4	Sequence 4, Appl
32	238	56.3	800	3	US-08-545-809A-39	Sequence 39, Appl
33	237.8	56.2	366	1	US-08-360-125-9	Sequence 9, Appl
34	237.8	56.2	366	2	US-08-450-578-9	Sequence 9, Appl
35	237.8	56.2	366	2	US-09-017-628-9	Sequence 9, Appl
36	237.8	56.2	366	2	US-09-014-880-9	Sequence 9, Appl
37	236.6	55.9	622	3	US-08-545-809A-59	Sequence 59, Appl
38	227.2	53.7	1418	4	US-08-793-450-7	Sequence 7, Appl
39	223.6	52.9	631	3	US-08-545-809A-31	Sequence 31, Appl
40	221.2	52.3	687	3	US-08-545-809A-34	Sequence 34, Appl
41	217.6	51.4	372	2	US-08-477-553A-46	Sequence 46, Appl
42	217	51.3	363	2	US-08-477-553A-50	Sequence 50, Appl
43	213.2	50.4	384	2	US-08-652-816A-20	Sequence 20, Appl
44	210	49.6	384	2	US-08-477-553A-49	Sequence 49, Appl
45	209.8	49.6	357	1	US-08-360-125-3	Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-08-803-085-2  
Sequence 2, Application US/08803085  
Patent No. 6011138  
GENERAL INFORMATION:  
APPLICANT: REFF, Mitchell E.  
APPLICANT: KLOETZER, William S.  
APPLICANT: NAKAMURA, Takaniko  
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWICKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22133-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/803,085  
FILING DATE: 20-FEB-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..423  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 58..423  
US-08-803-085-2

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; INFORMATION FOR SEQ ID NO: 11
;
; SEQUENCE CHARACTERISTICS:

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OPERATING SYSTEM: PC-DOS/MS-DOS









APPLICANT: RAAB, Ronald W.  
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P. O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22133-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,237  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-476-237-15

Query Match 70.5%; Score 298.2; DB 1; Length 423;  
Best Local Similarity 83.2%; Pred. No. 6,8e-78;  
Matches 352; Conservative 0; Mismatches 68; Indels 3; Gaps 1;

QY 1 ATGAACACCTGTTCTTCTCTCTCTGTCAGAGTCCGAGATGGTCTGCCAG 60  
DB 4 ATGAACACCTGTTCTTCTCTCTCTCTGTCAGAGTCCGAGATGGTCTGCCAG 63  
QY 61 CTGCACCTGCAGAGTGGGCGCCAGAGTGTGTAAGCCTTCGAGACCTGTCCTCAC 120  
DB 64 GTGCACCTGCAGAGTGGGCGCCAGAGTGTGTAAGCCTTCGAGACCTGTCCTCAC 123  
QY 121 TGGCGTGTCTGTGTGGTCTGTCAACAGTACTGGTGGACCTGGATCCCGACCC 180  
DB 124 TGCAGTGTCTGTGTGGTGTCCATCAACGCGGTGACTATTATTGTTGATCCCGACGTCC 183  
QY 181 CCAGGAGGAGTGTGATGATGAGATCTCTGATGAGTGGGCGCACCACTAC 240  
DB 184 CCAGGAGGAGTGTGATGATGAGATCTCTGATGAGTGGGCGCACCACTAC 243  
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DB 244 AATCCCTCCCTCAAGAGTGAAGTATTCATTCATGACAGTCCAAAGACGTTCTCC 303  
QY 301 CTGAACCTGAATCTGTGTGACCGCGGACACGCGGTATTACTGTGCCAGAGATTGG 360  
DB 304 CTGAACCTGAATCTGTGTGACCGCGGACACGCGGTATTACTGTGCCAGAGATTGG 360  
QY 361 GCCCAATATGCTGGAACAACAGCTAGGCTTCTGGGCGCAGAGTCTCTGTCACCGTCTCC 420  
DB 361 AATTGAATATCTTCATCTGTTATTATTACTGGGCGCAGAGTCTCTGTTCAACCGTCTCC 420

QY 421 TCA 423  
DB 421 TCA 423

RESULT 9  
US-08-478-039-107  
Sequence 107, Application US/08478039  
Patent No. 5681722  
GENERAL INFORMATION:  
APPLICANT: Newman, Roland A.  
APPLICANT: Hanna, Nabil W.  
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22133-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,039  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/379,072  
FILING DATE: 25-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/912,292  
FILING DATE: 10-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/856,281  
FILING DATE: 23-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/735,064  
FILING DATE: 25-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin Esq., Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-160  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 107:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 420 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Monkey  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Anti-CD4 VH  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 4..420  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 61..420  
US-08-478-039-107

Query Match 69.8%; Score 295.2; DB 1; Length 420;  
Best Local Similarity 83.1%; Pred. No. 5.1e-77;



Query Match	Similarity	69.8%	Score	295.2	DB 3:	Length	420;
Best Local	Similarity	83.1%	Pred.	N5.1e-77;			
Matches	349;	Conservative	0;	Mismatches	68;	Indels	3; Gaps
OY	1	ATGAAACACCTGTGGTTCCTCCTCCCTCGTGAGGCAGCTCCAGATGAGCTCTGCCAG	60				
Dd	4	ATGAACACACTGTGGTTCTCTCTCCCTCGTGAGGCAGCCCCAGATGGTCTTGTCCAG	63				
OY	61	CTGCAGCTGCAGGAAATCGGGGCCAGGAGTGGTGAAGCCTTGGAGACCCTGTCCAC	120				
Dd	64	GTCGAGCTGCAGGAGAGCGGGCCCAGAGACTGGTGAAGCCTTCGAGACCCTGTCCAC	123				
OY	121	TGCGCTGTCTGTGGTGGCTCTGTACAGAGTAATACTGGTGAACCTGGATCCGACGCC	180				
Dd	124	TGCATGTCTGTGGTGGCTCCATCAGCGGTGACTATTATGGTCTTGATTCGGCCAGTCC	183				
OY	181	CCAGGGAAGGAGCTGGAGTGGATTTGACGATATCTGTGATGGTGGGGCAACAATAC	240				
Dd	184	CCAGGGAAGGAGCTGGAGTGGATTTGACGATATTTGCAATGGCATGGTGGGGCACCAATAC	243				
OY	241	AACCGCTCCCTCAAGTGCAGTCAATTCATACAGAAGCAGCTCCAAGAACAGTTCTCC	300				
Dd	244	AATCCCTCCCTCAACATTCAGACTCTCCATTTTAAATAGACCTCCAGAACTCTTCTCC	303				
OY	301	CTGAACCTGAACCTGTGTACCGCCCGGACAGAGGCCGTGTATTACTGTCCAGAGATTGG	360				
Dd	304	CTGAACCTGAGAGTGTGTACCGCCCGGACAGAGGCCGTGTATTACTGTCCAGATAT---	360				
OY	361	GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCAGGAGTCCGTGCACCGCTCC	420				
Dd	361	ATATTGAATATCTTCACTGTTATTATACGTGGGCCAGGAGTCCGTGTCCACCGTCC	420				

1

	Query Match	69.1%	Score 292.4	DB 3	Length 1431	
	Best Local Similarity	81.5%	Pred. No. 5.1e-76			
	Matches 357	Conservative 0	Mismatches 66	Indels 15	Gaps 1	
QY	1	ATGAACACCTGTGGTCTTCTCCTCCTGTGTGAGCTCCAGATGGCTGTGCCAG	60			
Db	1	ATGAACACACGTGTGGTCTTCTCCTCCTGTGTGAGCTCCAGATGGCTGTGCCAG	60			
QY	61	CTGACGTGCAGAGATGTGGGCCAGAGATGTGAGACCTTGGAGACCTGTGCCACAC	120			
Db	61	GTGAAGCTGCAGACATGTGGGCCAGAGACTTCTGCAGCCTTGGAGACCTGTGCCACAC	120			
QY	121	TGCGCTGTCTGTGTGGCTGTGTCTGTCTGATAGTAAGTACTGGTGGACCTGTGATCCGACGCC	180			
Db	121	TGCGTGTCTGTGTGGCTGTGTCTGTCTGATAGTACTGGTGGACCTGTGATCCGACGCC	180			
QY	181	CCAGGAGGAAGGACATGTGATGTGACGTATCTGTGTGATGTGTGGGGCCACCAACTAC	240			
Db	181	CCAGGAGGAGGACATGTGATGTGACGTATCTGTGTGATGTGTGGGGCCACCAACTAC	240			
QY	241	AACCGGTCCCTCAAGAGTCAGATCATCTATTTCACACAGACGTCCCAAGACCAAGTTCAC	300			
Db	241	AATCCCTCCTCAAGAGTCAGATCATCTATTTCACCAAGACAGCTCCCAAGACCAAGTTCAC	300			
QY	301	CTGAACCTGAACCTGTGTACCGCGCGGACACAGGCGCGTATATTACTGTGCCAGAGATTGG	360			
Db	301	CTGAACCTGAACCTGTGTACCGCGCGGACACAGGCGCGTATATTACTGTGCCAGAGATTGG	360			





Oy	1	ATGAAACACCTGTGGTTCTTCTCTCTCTCTGCTGGACCTCCAGATGGGCTCTGCCAG	60
Dd	1	ATGAAACACCTGTGGTTCTTCTCTCTCTCTGCTGGACCTCCAGATGGGCTCTGCCAG	60
Oy	61	CTGACGCTCAGGAGTCGGGCCAGGAGTGGTGAAGCCTTGGAGACCTGTCCCTACC	120
Dd	61	GTGCACTACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTGGAGACCTGTCCCTACC	120
Oy	121	TGGCGTCTCTGTGGTGTCTGTACAGATGTAATCTGGTGGACCTTGGATTCGCCACGCC	180
Dd	121	TGGCGTCTCTGTGGTGTCTGTACAGATGTAATCTGGTGGACCTTGGATTCGCCACGCC	177
Oy	181	CCAGGAGGGGACCTGGAGTGGATTGGACGTATCTCTGGTATGGTGGGGCCACCACTAC	240
Dd	178	CCAGGTAGGGGCTGGAGTGGATTGGGGAATCAATATATGTGGAG---CACCACTAC	234
Oy	241	AACCCGTCTCCACAGAGTCGAGTATCATTTCCACACAGACAGTCCAGAACCGATTCTCC	300
Dd	235	AACCGTCTCCACAGAGTCGAGTATCATATCACTACACAGTCCAGAACCGATTCTCC	294
Oy	301	CTGAACCTGAACCTGTGACCGCGCGGACACGGCCGTGATTAACGTGGCCAGAGATTGG	360
Dd	295	CTGAAGCTGACCTGTGACCGCGCGGACACGGCCTGTGATTAACGTGGGAG-----	347
Oy	361	GCCCAATAGCTGGACCAACGCTTAGGCTTCTGGGGCCAGGAGAGTCTGTCACCGTCTCC	420
Dd	348	-----AGTAAATTAATTTGGTTCGACCCCTGGGGCCAGGGAACCGTGTACCGTCTCC	399
Oy	421	TCA 423	
Dd	400	TCA 402	

Search completed: September 23, 2002, 18:00:51  
Job time: 3222 sec





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:50:07 ; Search time 2581.68 Seconds  
(without alignments)  
3136.938 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387  
Sequence: 1 ATGACATGAGGCTCCCGC.....GACCAAGTGGAAATCAAA 387

Scoring table: IDENTITY NUC  
Gapop 10-0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
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19: em\_nu:\*  
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25: em\_pl:\*  
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27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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1	342.2	88.4	429	9	HUMIGKW	M74019 Homo sapien
2	342.2	88.4	729	6	E40896	E40896 Humanized a
3	334.2	86.4	390	9	MM057571	U57571 Macaca mula
4	334.2	86.4	396	6	E12918	E12918 Human mRNA
5	332.6	85.9	406	9	HUMIGKFN	M87478 Human reari
6	331.2	85.6	400	9	AF228327	AF228327 Homo sapi
7	330.8	85.5	432	9	HUMIGRVCA	L01279 Homo sapien
8	329.4	85.1	390	9	MM057579	U57579 Macaca mula
9	329.4	85.1	974	6	AX305000	AX305000 Sequence
10	329.4	85.1	974	6	AX306529	AX306529 Sequence
11	328.4	84.9	370	9	HSIGKLV20	X72441 H.sapiens m
12	326.2	84.3	396	9	HSPBLIGVD	Z27173 H.sapiens r
13	325.6	84.1	383	9	HSIGKLV56	X72477 H.sapiens m
14	323.6	83.6	389	9	HSIGKLV06	X72427 H.sapiens m
15	323	83.5	728	6	AX327729	AX327729 Sequence
16	321.4	83.0	388	9	HSTR0IGVJ	X85997 H.sapiens m
17	321.4	83.0	390	9	HSR0G31L	X64163 H.sapiens m
18	321.4	83.0	441	9	HSU43767	U43767 Human Immun
19	321.4	83.0	716	6	AX327727	AX327727 Sequence
20	321.2	83.0	650	9	HS4010446	AJ010446 Homo sapi
21	319.4	82.5	399	9	HSIGKLV23	X72444 H.sapiens m
22	318.2	82.2	388	6	AR161375	AR161375 Sequence
23	315	81.4	390	9	HSU43773	U43773 Human Immun
24	314.6	81.3	369	9	HSIGKLV02	X72423 H.sapiens m
25	313.8	81.1	395	9	HSIGKLV41	X72462 H.sapiens m
26	313.4	81.0	388	9	HSDDELIGVJ	X85995 H.sapiens m
27	313.4	81.0	388	9	HSTR0IGVJ	X85996 H.sapiens m
28	313.4	81.0	953	9	BC005332	BC005332 Homo sapi
29	313	80.9	388	9	HSIGKLV58	X72479 H.sapiens m
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31	311.8	80.6	387	9	MM057574	U57574 Macaca mula
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33	311.8	80.6	393	9	HUMIG6L	L38434 Homo sapien
34	311.8	80.6	698	6	AX327725	AX327725 Sequence
35	311.8	80.6	944	6	AX067344	AX067344 Sequence
36	310.4	80.2	370	9	HSIGKLV03	X72424 H.sapiens m
37	310.2	80.2	390	9	HS1AM007	Z68958 H.sapiens m
38	308.8	79.8	523	6	AX340963	AX340963 Sequence
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40	308.6	79.7	433	9	S59162	S59162 Ig V kappa
41	308.4	79.7	351	9	S67637	S67637 Homo sapien
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43	307	79.3	439	6	AR161377	AR161377 Sequence
44	306.8	79.3	393	9	HUMIGKBA	M33060 Human Ig re
45	306.4	79.2	384	9	HSPOM016	Z68992 H.sapiens m

## ALIGNMENTS

RESULT	1	LOCUS	HUMIGKW	DEFINITION	Homo sapiens immunoglobulin light chain variable region (IGLE)	ACCESSION	M74019.1	GI:186042	VERSION	M74019	KEYWORDS	SOURCE	ORGANISM	human.	REFERENCE	1 (bases 1 to 429)	AUTHORS	Moore,J.S., Nowell,P.C., Roelcke,D., Pruzanski,W., Roudier,J. and Silverman,G.J.	TITLE	Variable region gene analysis of pathologic human autoantibodies to blood (1991) In press	JOURNAL	Location/Qualifiers	FEATURES	source		
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1..>429 /gene="IGL@"  
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V\_region /gene="IGL@"

BASE COUNT 104 a 122 c 102 g 101 t

ORIGIN

Query Match 88.4%; Score 342.2; DB 9; Length 429;  
Best Local Similarity 92.8%; Pred. No. 2.6e-101;  
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGTCTCGGGGCTCTTCTGCTGCTGCTCCAGGTGCC 60  
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DB 1 ATGGACATGAGGGTCCCGCTCAGTCTCGGGGCTCTTCTGCTGCTGCTCCAGGTGCC 60  
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DB 181 AAACCAAGAAAGCTCTTAAGTCTGATCTATGTCATCCAGTTCGAAAGTGGGGTC 240  
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DB 241 CCATCAAGGTTTCAGGGCAAGTGTGAGACAGAGTTCACCTCAGCAGAGCTG 300  
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QY 361 GGCCAAGGACCAAGGTGGAATCAAA 387  
1 GGCCAAGGACCAAGGTGGAATCAAA 387  
DB 361 GGCCAAGGACCAAGGTGGAATCAAA 387

RESULT 2  
LOCUS E40896 729 bp DNA linear PAT 31-JAN-2002  
DEFINITION Humanized anti-Fas antibody.  
ACCESSION E40896  
VERSION E40896.1 GI:18627473  
KEYWORDS JP 200016574-A/85.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 729)  
AUTHORS Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.  
TITLE Humanized anti-Fas antibody  
JOURNAL Patent: JP 200016574-A 85 20-JUN-2000;  
OS SANKYO CO LTD  
COMMENT O5 Homo sapiens (human)  
PN JP 200016574-A/85

PD 20-JUN-2000 1999275441  
PF 29-SEP-1999 JP 1999275441  
PR NOBURI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKURO TAMAKI  
PI C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,  
PC C07K16/18,  
PC C12N1/21,C12N5/10,C12P21/08//C12N1/21,C12N1/19,C12N15/00, PC  
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FH Key Location/Qualifiers  
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FEATURES Location/Qualifiers  
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BASE COUNT 192 a 200 c 182 g 155 t

ORIGIN

Query Match 88.4%; Score 342.2; DB 6; Length 729;  
Best Local Similarity 92.8%; Pred. No. 2.7e-101;  
Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGTCTCGGGGCTCTTCTGCTGCTGCTCCAGGTGCC 60  
1 ATGGACATGAGGGTCCCGCTCAGTCTCGGGGCTCTTCTGCTGCTGCTCCAGGTGCC 60  
DB 7 ATGGACATGAGGGTCCCGCTCAGTCTCGGGGCTCTTCTGCTGCTGCTCCAGGTGCC 66  
QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGCTGCTGCTGAGGACAGA 120  
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DB 67 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGCTGCTGCTGAGGACAGA 126  
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1 GTCACATCATCTGCAGGCAAGTCAAGACATTAATTAATGATCAAGACAG 180  
DB 127 GTCACATCATCTGCAGGCAAGTCAAGACATTAATTAATGATCAAGACAG 186  
QY 181 AAACCAAGAAAGCTCTTAAGTCTGATCTATGTCATCCAGTTCGAAAGTGGGGTC 240  
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DB 187 AAACCAAGAAAGCTCTTAAGTCTGATCTATGTCATCCAGTTCGAAAGTGGGGTC 246  
QY 241 CCATCAAGGTTTCAGGGCAAGTGTGAGACAGAGTTCACCTCAGCAGAGCTG 300  
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DB 247 CCATCAAGGTTTCAGGGCAAGTGTGAGACAGAGTTCACCTCAGCAGAGCTG 306  
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1 CAGCTGGAAGATTTTGCAGATTATTAAGTCTGACAGTTATAGTACCCCTCGAGCTTC 360  
DB 307 CAGCTGGAAGATTTTGCAGATTATTAAGTCTGACAGTTATAGTACCCCTCGAGCTTC 366  
QY 361 GGCCAAGGACCAAGGTGGAATCAAA 387  
1 GGCCAAGGACCAAGGTGGAATCAAA 387  
DB 367 GGCCAAGGACCAAGGTGGAATCAAA 393

RESULT 3  
LOCUS MM057571 390 bp mRNA linear PRI 02-OCT-1996  
DEFINITION Macaca mulatta Ig rearranged light chain variable region, anti-RBC  
antibody, mRNA, partial cds.  
ACCESSION U57571  
VERSION U57571.1 GI:1575089  
KEYWORDS  
SOURCE Rhesus monkey.  
ORGANISM Macaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecidae; Macaca.  
REFERENCE 1 (bases 1 to 390)  
AUTHORS Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.  
and Capra,J.D.  
TITLE Variable Region Gene Segment Utilization in Rhesus Monkey  
Hybridomas Producing Human Red Blood Cell-Specific Antibodies:  
Predominance of the VH4 Family but not VH4-21 (V4-34)  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 390)  
 AUTHORS Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,  
 University of Texas Southwestern Medical Center, 6000 Harry Hines  
 Blvd., Dallas, TX 75235-9140, USA  
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 BASE COUNT 97 a 108 c 94 g 91 t  
 ORIGIN

Query Match 86.4%; Score 334.2; DB 9; Length 390;  
 Best Local Similarity 91.5%; Pred. No. 1.1e-98;  
 Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGAGGCCCCCTCAGCTCTCGGGGCTCTGCTGCTGCTCCAGGTCC 60  
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 DB 1 ATGGACATGAGGAGGCCCCCTCAGCTCTCGGGGCTCTGCTGCTGCTCCAGGTCC 60  
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 QY 61 AGATGTGACATCCAGATGAGACCAAGTCTCCATCTCCCTGTGACATCTGTAGGGAGACA 120  
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 DB 61 AGATGTGACATCCAGATGAGACCAAGTCTCCATCTCCCTGTGACATCTGTAGGGAGACA 120  
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 QY 121 GTACACATCACTTGGACGGGCAAGTGCAGACATTAGTATTAATTGATTCAGACAG 180  
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 DB 121 GTACACATCACTTGGACGGGCAAGTGCAGACATTAGTATTAATTGATTCAGACAG 180  
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 QY 181 AAACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240  
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 DB 181 AAACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240  
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 QY 241 CCATCAAGTTGACGGCGCAGTGTGATGGACAGAGTTCACTCTACCGTCAGACAGCTG 300  
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 DB 241 CCATCAAGTTGACGGCGCAGTGTGATGGACAGAGTTCACTCTACCGTCAGACAGCTG 300  
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 QY 301 CAGCCTGAGATTTTGGGACTATTACTGTCTACAGGTTTATAGTACCCTCGAGAGTTC 360  
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 DB 301 CAGCCTGAGATTTTGGGACTATTACTGTCTACAGGTTTATAGTACCCTCGAGAGTTC 360  
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 QY 361 GGCCAGGAGCAAGGTGAAATCAAA 387  
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 DB 361 GGCCAGGAGCAAGGTGAAATCAAA 387  
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RESULT 4  
 LOCUS E12918 396 bp DNA linear PAT 24-JUN-1998  
 DEFINITION Human mRNA for variable region of light chain of anti-carcinoma  
 monoclonal antibody CLN'1-1gM, complete cds.  
 ACCESSION E12918  
 VERSION E12918.1 GI:3251749  
 KEYWORDS JP 1997100300-A/2.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 396)  
 AUTHORS Hagihara, H., Aozuka, Y., and Miyahara, J.  
 TITLE AMINO ACID SEQUENCE OF ANTICANCER HUMAN MONOCLONAL ANTIBODY AND DNA  
 BASE SEQUENCE CODING FOR THE SAME

JOURNAL Patent: JP 1997100300-A 2 15-APR-1997;  
 COMMENT HAGIWARA YOSHITIDE  
 OS Homo sapiens (human)  
 PN JP 1997100300-A/2  
 PD 15-APR-1997  
 PE 03-OCT-1995 JP 1995278266  
 PI HAGIWARA HIDEAKI, AOZUKA YASUYUKI, MIYAHARA JUNICHI PC  
 C07R16/42, C07H21/04, C12N15/02, C12N15/09, A61K39/395, C12N5/10, PC  
 C12P21/08,  
 PC G01N33/53, G01N33/574, G01N33/577;  
 CC strandedness: Double;  
 CC topology: Linear;  
 FH key Location/Qualifiers  
 FH source 1. .396  
 FT /organism='Homo sapiens'  
 FT /cell\_type='hybridoma cell'  
 FT /cell\_line='HT-2'  
 FT sig\_peptide 1. .66  
 FT mcl\_peptide 67. .396  
 FT /product='variable region of light chain of  
 FT anti-carcinoma  
 FT monoclonal antibody CLN'1-1gM' FT  
 FT misc\_feature 136. .168  
 FT /note='this region encodes Complementarity FT  
 FT determining region (CDR1)'  
 FT misc\_feature 214. .234  
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 FT determining region (CDR2)'  
 FT misc\_feature 331. .348  
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 FT determining region (CDR3)'.  
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 BASE COUNT 101 a 107 c 97 g 91 t  
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 Best Local Similarity 91.5%; Pred. No. 1.1e-98;  
 Matches 354; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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 QY 61 AGATGTGACATCCAGATGAGACCAAGTCTCCATCTCCCTGTGACATCTGTAGGGAGACA 120  
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 DB 61 AGATGTGACATCCAGATGAGACCAAGTCTCCATCTCCCTGTGACATCTGTAGGGAGACA 120  
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 QY 121 GTACACATCACTTGGACGGGCAAGTGCAGACATTAGTATTAATTGATTCAGACAG 180  
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 DB 121 GTACACATCACTTGGACGGGCAAGTGCAGACATTAGTATTAATTGATTCAGACAG 180  
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 QY 181 AAACGAGGAAAGCTCCTAAGCTCTGATCTATGTTGATCCAGTTTGCAAGTGGGGTC 240  
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 QY 241 CCATCAAGTTGACGGCGCAGTGTGATGGACAGAGTTCACTCTACCGTCAGACAGCTG 300  
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 DB 241 CCATCAAGTTGACGGCGCAGTGTGATGGACAGAGTTCACTCTACCGTCAGACAGCTG 300  
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 QY 301 CAGCCTGAGATTTTGGGACTATTACTGTCTACAGGTTTATAGTACCCTCGAGAGTTC 360  
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 DB 301 CAGCCTGAGATTTTGGGACTATTACTGTCTACAGGTTTATAGTACCCTCGAGAGTTC 360  
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 QY 361 GGCCAGGAGCAAGGTGAAATCAAA 387  
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Db      361  GGCCAAGGACCAAGGTGGAATCAAA 387

RESULT  5
LOCUS   HUMIGKFN      406 bp      mRNA      linear      PRI 28-OCT-1994
DEFINITION Human rearranged Igk mRNA VJC region.
ACCESSION M87478
VERSION  M87478.1 GI:185950
KEYWORDS C-region; J-region; V-region; immunoglobulin kappa-chain;
SOURCE   immunoglobulin light chain.
         Homo sapiens (individual isolate patient CHEB) bone marrow CDNA to
         mRNA.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 406)
AUTHORS   Auccutner, P., Bauwens, M., Khmalich, A.A., Denoey, L.,
           Splenelli, S., Touchard, G., Preud'homme, J.L. and Cogne, M.
           Monoclonal Ig L chain and L chain V domain fragment crystallization
           in myeloma-associated Fanconi's syndrome
JOURNAL   J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)
MEDLINE   93224763
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Best Local Similarity 91.2%; Pred. No. 3.8e-98;
Matches 353; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY      1  ATGACATGAGGTCCTCCGCTCAGCTCCTGCGGCTCTTCTGCTGCGTCCAGGTGCC 60
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DB      2  ATGACATGAGGTCCTCCGCTCAGCTCCTGCGGCTCTTCTGCTGCGTCCAGGTGCC 61

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QY      61  AGATGTGACATCCAGATGAGCCAGTCTCCATCTCCCTGTGTCATCTGTAGGGACAGA 120
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QY      121  GTACCATCTACTGTCAGGGCAGACATGACGACATTAGTATTATTAATGTGTCAGCAG 180
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DB      122  GTACCATCTACTGTCAGGGCAGACATGACGACATTAGTATTATTAATGTGTCAGCAG 181
QY      181  AAMCCAGAAAGCTCCTTAAGCTCTGATCTATGTGATCCAGTTCGCAAGTGGGGTC 240
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DB      182  AAMCCAGGGAAGCCCTTAAGCTCTGATCTATGTGATCCAGTTCGCAAGTGGGGTC 241
QY      241  CCATCAAGGTTCAGCGCAGTGTGATCTGGACAGAGTTCACTTCACCGTCAGCAGCTG 300
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DB      242  CCATCAAGGTTCAGTGTGATCTGGACAGAGTTCACTTCACCATACAGCAGCTG 301
QY      301  CAGCTGAAGATTTTGCAGTTATTACTGTCTACAGTTATAGTACCCCTGGAGCTTC 360
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DB      302  CAACCTGAAGATTTTCACTTCACTGTCAACAGAGTTACGATCCCGGTGAGCTTC 361
QY      361  GGCCAAGGACCAAGGTGGAATCAAA 387
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DB      362  GGCCAAGGACCAAGGTGGAATCAAA 388

RESULT  6
AF228327
LOCUS   AF228327      400 bp      DNA      linear      PRI 20-JUL-2000
DEFINITION Homo sapiens clone BUS immunoglobulin light chain variable region
ACCESSION AF228327
VERSION  AF228327.1 GI:9295292
KEYWORDS gene, partial cds.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS   Maloum, K., Dighiero, G. and Magnac, C.C.
           Unmutated Ig VH genes in CLL patients
JOURNAL   Unpublished
TITLE     2 (bases 1 to 400)
AUTHORS   Maloum, K., Dighiero, G. and Magnac, C.C.
           Direct Submission
           Submitted (13-JAN-2000) Physiopathology, Institut Pasteur, 28 rue
           du Dr Roux, Paris 75015, France
JOURNAL
FEATURES
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            /db_xref="taxon:9606"
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BASE COUNT 99 a 109 c 100 g 92 t
ORIGIN
Query Match      85.6%; Score 331.2; DB 9; Length 400;
Best Local Similarity 91.4%; Pred. No. 1.1e-97;

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JOURNAL	Submitted (03-NOV-1993) M. Zouali, Institut Pasteur, Immunogenetique Cellulaire, 28 Rue du Dr. Roux, 75015 Paris, FRANCE
REFERENCE	3 (bases 1 to 396)
AUTHORS	Bensimon, C., Chastagner, P. and Zouali, M.
TITLE	Human lupus anti-DNA autoantibodies undergo essentially primary V kappa gene rearrangements
JOURNAL	EMBO J 13 (13), 2951-2962 (1994)
MEDLINE	94313975
FEATURES	Location/Qualifiers 1..396 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_line="T21-9" /cell_type="PBL" CDS 1..>396 /codon_start=1 /product="Ig light chain variable region (VJ)" /protein_id="CAA81697.1" /db_xref="GI:415962" /translation="HSDMRVPAQLDLLELLMLPGACAIRIAOSPSSLASTGDRVT ITPCASOGISSLAYOQKPKAPAKRLIYASTLQSGVPSFSGSGSTPFTLISCL QSEDFATPYCCQVYSYPRTEGQKVEIKR" V_region V_segment 73..357 /note="VK1" J_segment 358..396 /note="JK1" BASE COUNT 95 a 112 c 96 g 93 t ORIGIN
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Db	7 ATGGACATGAGGGTCCCGGCTCAGCTCCTGGGGCTTCCTGCTCTGGCTCCAGATGCC 66
QY	61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTGATCTGTAGGGGACAGA 120
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QY	121 GTCACTCATCTACTGCAAGGCGAAGTCAAGCAATTAAGTATTAATTGGTATCAGCAG 180
Db	127 GTCACTCATCTACTGCGGCGAGTCAAGGAGTATTAAGCAATTAATTAGCCTGTATCAGCAA 186
QY	181 AAACGAGAAAAAGCTCCTTAAGCTCCTGATCTATGTGTGATCCAGTTGGCAAGTGGGCTC 240
Db	187 AAACGAGGAAAAAGCTCCTTAAGCTCCTGATCTATGTGTGATCCAGTTGGCAAGTGGGCTC 246
QY	241 CCATCAAGGTTCAAGGCGAGTGAATCTGGAGCAGAGTCACTCACGCGTCAGCAGGCTG 300
Db	247 CCATCAAGGTTCAAGGCGAGTGAATCTGGAGCAGATTTCACTCTCACCATCAGCTGCTG 306
QY	301 CAGCTGAAGATTTTTCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTC 360
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QY	361 GGCCTAAGGAGGACCAAGGTGAAATCAA 387
Db	367 GGCCTAAGGAGGACCAAGGTGAAATCAA 393
RESULT 13	
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LOCUS	HSIGKLV56 383 bp mRNA linear PRI 31-JAN-1994
DEFINITION	H.sapiens mRNA for rearranged ig kappa light chain variable region
ACCESSION	X72477.1
VERSION	X72477.1
KEYWORDS	C-region; Immunoglobulin; J-segment; kappa light chain; V-region.
human	

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 383)
TITLE	Zachau, H. G.
JOURNAL	Submitted Direct Submission
REFERENCE	Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2, FRG
AUTHORS	2 (bases 1 to 383)
TITLE	Klein, R., Jaenichen, R. and Zachau, H. G.
JOURNAL	Expressed human immunoglobulin kappa genes and their hypermutation
REFERENCE	Eur. J. Immunol. 23 (12), 3248-3262 (1993)
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136	AGGCGAAGTCAGAGCATTTAGTATTATTTAAATGTGATTCAGACAGAAACAGAGAAAGCT 195
121	CGGCGAAGTCAGAGCATTTAGTATTATTTAAATGTGATTCAGACAGAAACAGAGAAAGCT 180
196	CCTAAGCTTCGATGTATGTGATCCAGTTTGCAAGATGGGGGTCCTCAAGGTTCCAGC 255
181	CCTAAGCTTCGATGTATGTGATCCAGTTTGCAAGATGGGGGTCCTCAAGGTTCCAGC 240
256	GGCAGTGGATGTGGAGACAGATTCACCTTCACCGTCAGACAGACCTTCGAGATTTT 315
241	GGCAGTGGATGTGGAGACAGATTTACCTTCACCGTCAGACAGACCTTCGAGATTTT 300
316	GCGACTTATCTGTCTACAGGTTTATAGTACCCCTCGAGAGTTTCGGCCAAAGGACCAAG 375
301	GCAACTTACTACTGTCACACAGAGTTTACAAATACCCCGTGGAGGTTTCGGCCAAAGGACCAAG 360
376	GTGGAATCAAA 387
361	GTGGAATCAAA 372



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DEFINITION H.sapiens mRNA for rearranged Ig kappa light chain variable region
            (I.45).
ACCESSION X72427.1 GI:441322
VERSION X72427
KEYWORDS Immunoglobulin; J-segment; kappa light chain; V-region.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 389)
AUTHORS Zachau, H.G.
TITLE Direct Substitution
JOURNAL Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische
            Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2,
            FRG
FEATURES
    REFERENCE 2 (bases 1 to 389)
    AUTHORS Klein, R., Jaenichen, R., and Zachau, H.G.
    TITLE Expressed human immunoglobulin kappa genes and their hypermutation
    JOURNAL Eur. J. Immunol. 23 (12), 3248-3262 (1993)
    MEDLINE 94080891
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Matches 347; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
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DB 61 GATGTGATCCAGATGACCCAGTCTCCATCTTCCCTGTGCTGCTGTAGGGACAGAG 120
QY 122 TCACCATCATCTTGGCGGCAAGTTCAGACATTTAAATTGGATCAGCAGA 181
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    |||||||
DB 181 AACGAGAAAGCTCTTACCTCTGATCTATGTTCATCAGTTTCAAAAGTGGGCTCC 240
QY 242 CATCAAGGTTGAGGAGGATGATCTGGACAGAGTTCACTTCACCGGTGACGACGCTGC 301
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DB 301 AACCTGAGATTTTGGAGCTATTTACTGTTTACTACAGGTTTACTACCCCGAGCGTTGG 360
QY 362 GCCAAGGAGCAAGTGTGAATCAAA 387
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DB 361 GCCAAGGAGCAAGTGTGAATCAAA 386
RESULT 15
LOCUS AX327729 728 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 15 from Patent WO0183755.
ACCESSION AX327729
VERSION AX327729.1 GI:18098040
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Mikayama, T., Takahashi, N., Chen, X., and Schoenberger, S.P.
TITLE Human anti-cd40 antibodies and methods of making and using same
JOURNAL Patent: WO 0183755-A 15 08-NOV-2001;
            Gemini Science, Inc. (US)
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Best Local Similarity 89.7%; Pred. No. 5.6e-95;
Matches 347; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGCTGAGTCCAGGTGCC 60
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DB 59 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTCTGCTGCTGAGTCCAGGTGCC 118
QY 61 AGATGTGACATTCAGATGACCCAGTCTCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
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DB 119 AGATGTGACATTCAGATGACCCAGTCTCATCTTCCCTGTCTGCATCTGTAGGGACAGA 178
QY 121 GTACCATCTACTTGACAGGCAAGTCAAGACATTAGTATTATTTAAATTGATCAGCAG 180
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DB 179 GTACCATCTACTTGCTGGGGAGTCAAGGATTTAGCAGCTGTAGGCTGTATTCAGCAG 238
QY 181 AACCCAGAAAGCTCTTAGCTCTGATCTATGCTGATCCAGTTTGCAAAATGGGGTCC 240
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QY 241 CCATCAAGTTTCAGCGGCACTGTGAGACAGAGTTTCACTTCACCGTCCAGACCTTG 300
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DB 299 CCATCAAGTTTCAGCGGCACTGTGAGACAGAGTTTCACTTCACCGTCCAGACCTTG 358
QY 301 CAGCTGAAAGTTTGGAGCTTATTTACTGTCTCAGAGTTTAAATGATCCTCGGAGCTTC 360
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DB 359 CAGCTGAAAGTTTGGAGCTTATTTACTGTCAACAGGCTAGCAGTTTCCCTCGAGATTTC 418
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGGACATGAGGCTCCCGC.....GGACCAAGTGGAAATCATA 387

Scoring table: IDENTITY\_NUC

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Searched: 13736207 segs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estinu:\*  
5: em\_estrov:\*  
6: em\_estropl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	332.6	85.9	891	9	BG540787 602570674
3	329.6	85.2	724	10	BG537031 602565115
4	329.4	85.1	867	10	BG754732 602714301
5	329.4	85.1	886	10	BG756818 602710291
6	327.8	84.7	864	9	BG548281 602575248
7	326.6	84.4	391	9	AM404992 UT-HF-BL0
8	326.2	84.3	453	9	AM383563 PM4-HT034
9	324.6	83.9	447	9	AM405752 UT-HF-BL0
10	321.6	83.1	669	10	BG541198 602569978
11	321.4	83.0	770	10	BG688444 602637305
12	321.4	83.0	943	10	BG976230 602245105
13	321.4	83.0	1100	10	BG663472 602144635
14	320.6	82.8	712	10	BG538665 602566902
15	320.6	82.8	921	10	BG341239 602463904
16	319	82.4	557	10	BG760164 602733253
17	319	82.4	1038	10	BG757218 602710391

18	318.8	82.4	655	10	BG569796 602590416
19	318.8	82.4	858	10	BG756326 602713645
20	318.2	82.2	867	10	BG539961 602567476
21	318.2	82.2	872	10	BG535392 602563053
22	317.6	82.1	437	9	AM404458 UT-HF-BL0
23	317.4	82.0	817	10	BG432453 602495486
24	317.2	82.0	471	9	AM406284 UT-HF-BL0
25	317	81.9	566	9	AM406081 UT-HF-BL0
26	316.8	81.9	927	10	AV683828 AV683828
27	316.8	81.9	420	9	BG536845 602566383
28	316.6	81.8	755	10	BG533970 602553071
29	316.6	81.8	921	10	BG758398 602712592
30	316.2	81.7	431	9	AM406886 UT-HF-BL0
31	315.6	81.6	472	9	AM406323 UT-HF-BL0
32	315	81.4	680	9	AV733319 AV733319
33	315	81.4	711	10	BG546866 602574048
34	315	81.4	920	10	BG740562 602633076
35	314	81.1	813	10	BG431143 602498773
36	313.4	81.0	487	9	AM405988 UT-HF-BL0
37	313	80.9	714	10	BG757897 602714329
38	313	80.9	750	10	BG755394 602713951
39	311.8	80.6	721	10	BG686441 602638377
40	311.8	80.6	727	10	BG684242 602635874
41	311.8	80.6	744	10	B1761857 603048792
42	311.4	80.5	706	10	BG759950 602733557
43	311.4	80.5	1130	10	BG662874 602144820
44	311	80.4	688	10	BG539229 602567825
45	311	80.4	851	10	BG686018 602638582

## ALIGNMENTS

RESULT 1  
LOCUS AM405753 493 bp mRNA linear EST 16-FEB-2000  
DEFINITION UT-HF-BL0-abp-a-02-0-UT-1 NIH-MGC\_37 Homo sapiens cDNA clone  
IMAGE:3057290 5', mRNA sequence.  
ACCESSION AM405753  
VERSION AM405753.1 GI:6924810  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/  
1 (bases 1 to 493)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/dbp/image/image.html  
Seq primer: M3 Forward.  
Location/Qualifiers  
1. 493  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3057290"  
/clone\_lib="NIH-MGC\_37"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: pT73-Pac; site1: NotI; site2: Eco RI;  
constructed from size fractionated cytoplasmic mRNA  
(1.5-2.5kb). Directionally cloned. Cells provided by Louis

## FEATURES

source

BASE COUNT	117 a	138 c	119 g	119 t
ORIGIN	M. Staudt, Ph.D. Library preparation by Maria de Fátima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."			

Query Match	88.7%;	Score 343.4;	DB 9;	Length 493;
Best Local Similarity	93.2%;	Pred. No. 4.8e-94;		
Matches 359; Conservative	0;	Mismatches 26;	Indels 0;	Gaps 0

**Oy**    3 GGACATGAGGGTCCCCCCTCAGCTCCTGGGGCTCCTTTCTGTCTGGCTCCAGAGTGCCAG 62  
        |||||  
**Db**    8 GGACATGAGGGTCCCCTCAGTTCCTGGGGCTCCTGCTACTCTGGCTCCGAGAGTGCCAG 67

0y 63 ATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGGGACAGAGT 12  
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Db 68 ATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTGTAGGAGACAGAGT 12

Oy 123 CACCATCATTGCAAGGCAAGTCAGACATTAGGTAATTATTTAAATTGGTATCAGCAGAA 18  
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 Db 128 CACCATCATTGCGGCGCAAGTCAGAGACATTAGCAGCTATTTAAATTGGTATCAGCAGAA 18  
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Oy 183 ACCAAGGAAAACTCCCTAAAGCTCCTGATCTATGTTCATCCAGTTTGCAAGTGGGGTCCC 24  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 188 ACCAAGGAAGCCCCCTAAAGCTCCTGATCTATGTTCATCCAGTTTGCAAGTGGGGTCCC 24

Oy 243 ATCAAGGTTACGGCGAGTGGATCTGGGACAGAGTTACATCTTCACCGTCAGACGCTGCA 30  
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Db 248 ATCAAGGTTACGTGGCAGTGGATCTGGGACAGATTTCACCTTCACCATCAGCAGCTGCA 30  
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[illegible]

QY	363	CCAAGGACCAAGGTGGAATCAAA	387
Db	368	CCAAGGACCAAGGTGGAATCAAA	392

RESULT	2
RG540787	

DEFINITION	602570674E1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695114 mRNA sequence.
ACCESSION	BC540787

KEYWORDS	EST.
ORGANISM	human.
SOURCE	Homo sapiens

**REFERENCE**  
AUTHORS  
Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.  
1 (bases 1 to 891)  
NIH-MGC <http://mqc.nci.nih.gov/>.

**FILE** National Institutes of Health, mammalian gene collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Issue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 plate: 11CM1520 row: 6 column: 10

FEATURES	High quality sequence stop: 577.
source	Location/Qualifiers
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	/correlation: "These conditions"

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/clone="IMAGE:4695114"
/clone_1lp="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"

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BASE COUNT	CA). Note: this is a NIH-MGC Library."
239 a	248 c
237 g	167 t
ORIGIN	

Query Match	85.9%	Score 332.6;	DB 10;	Length 891;
Best Local Similarity	91.2%	Pred. No. 1.3e-90;		
Matches 353;	Conservative 0;	Mismatches 34;	Indels 0;	Gaps 0;

26 ATGGACATGAGGCTCCCGCTAGCTCTGAGGCTCCTCTGCTCTGGCTCCCAAGTCC 85  
 85

QY 61 AGATGTGACATCCAGATGACCCAGCTCTCCATCTCTCCCTGTCTGCATCTGTATGGGACAGA 120  
Db 86 AGATGTGACATCCAGTGTGACCCAGCTCTCCATCTCTCCCTGTCTGCATCTGTATGGAGACAGA 145

QY 121 GTCACCATCAGCTTGGCAGGCGCACTCAGACCATTAAGTATTATTAAATTGGTATCAGCAG 180

Db 146 GTCACCATCAGCTTGGCAGGCGCACTCAGACCATTAAGTATTATTAAATTGGTATCAGCAG 205

QY 181 AAACACAGAAAAGCTCTCTAAGCTCCTGATCTCTATGTTGCATCCAGTTCAGTTCAAAAGTGGGGTTC 240

Db 206 AAACACAGGAAAGCCCCCTTAAGATTTCTATCTCTATGCTGCATCCACTTTCACAAAGTGGGGTTC 265

QY	241	CCATCAAGCTTCAGCGCGCAGTGGATCTGGGACAGAGTTCACTTCACCGTCAACAGCCTG	300
Db	266	CCATCAAGTTTCAGCGCGCAGTGGATCTGGGACAGAAATTCACCTTCACATCAACAGCCTG	325

QY	301	CAGCCTTAAAGATTTTGGCAGCTTATTACTGTGTACACAGGTTTAAATAGTACCCCTCGAGCTTC	360
Db	326	CAGCCTTAAAGATTTTGGCAGCATTACTGTGTCAACAGCTTAATCTTATCTTCGAGACTTC	385

<b>Q7</b>	361	GGCCAAGGACCACAGTGGAAATCMAA	387
<b>D6</b>	386	GGCCAAGGACCACAGTGGAAATCMAA	412

RESULT	3
BG537031	

ACCESSION	BG537031				
DEFINITION	6025651151 NIH_MGC_77	1,24 bp	1 LINEAR	EST 03 APR 2000	
	Homo sapiens CDNA				
	clone IMAGE:4689963	5'			
	mRNA sequence.				

ORGANISM	Homo sapiens
SOURCE	human.
KEYWORDS	
EST.	
VERSION	B633/031.1
GI	13326379

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NIH-MGC <http://mgs.nci.nih.gov/>  
 1 (bases 1 to 724)  
 REFERENCE  
 AUTHORS

TITLE	JOURNAL	COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:corabbe-remail@nih.gov">corabbe-remail@nih.gov</a>

Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Data Secured by: The I.M.A.G.E. Consortium (LLNL)

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LILCM1506 row: m column: 04

High quality sequence stop: 573.

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source Location/Qualifiers

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4689863"
/clone_lib="NIH_MGC_77"
/lab_host="PH10B (p1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcgctcgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATATGAGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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BASE COUNT 190 a 204 c 181 g 149 t  
ORIGIN

Query Match 85.2%; Score 329.6; DB 10; Length 724;

Best Local Similarity 92.3%; Pred. No. 9.5e-90; Indels 1; Gaps 1;

Matches 358; Conservative 0; Mismatches 29; Indels 1; Gaps 1;

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DB 25 ATGACATGAGGCTCCCGCTCAGCTCTGCGGCTCTTCTGCTGCTGCTCCAGGTGCC 84

OY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTGAGGGACAGA 120

DB 85 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTGAGGGACAGA 144

OY 121 GTACCATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180

DB 145 GTACCATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 204

OY 181 AAACCAAGAAAGGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGAAGTGGGGTC 240

DB 205 AAACCAAGAAAGGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGAAGTGGGGTC 264

OY 241 CCATCAAA-GGTTGAGGCGGAGTGATCTGGGACAGAGTACTCTACCGTCAGACGCT 299

DB 265 CCATCAAAAGGTTGAGGCGGAGTGATCTGGGACAGAGTACTCTACCGTCAGACGCT 324

OY 300 GCAGCCGAAAGTTTGGCGATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 359

DB 325 GCAGCCGAAAGTTTGGCGATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 384

OY 360 CGGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 387

DB 385 CGGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 412

RESULT 4

LOCUS BG754732 867 bp mRNA linear EST 15-MAY-2001

DEFINITION 602714301F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4654409 5',

ACCESSION BG754732

VERSION BG754732.1 GI:14065385

KEYWORDS

SOURCE

ORGANISM

human  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 867)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabs@email.nih.gov](mailto:cgabs@email.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCMI702 row: a column: 02

High quality sequence stop: 805.

Location/Qualifiers

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:4654409"

/clone\_lib="NIH\_MGC\_48"

/tissue\_type="primary B-cells from tonsils (cell line)"

/lab\_host="PH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOTB; Site\_1: XhoI;

Site\_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

BASE COUNT 225 a 245 c 215 g 182 t  
ORIGIN

Query Match 85.1%; Score 329.4; DB 10; Length 867;

Best Local Similarity 90.7%; Pred. No. 1.2e-89; Indels 0; Gaps 0;

Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

OY 1 ATGACATGAGGCTCCCGCTCAGCTCTGCGGCTCTTCTGCTGCTGCTCCAGGTGCC 60

DB 19 ATGACATGAGGCTCCCGCTCAGCTCTGCGGCTCTTCTGCTGCTGCTCCAGGTGCC 78

OY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTGAGGGACAGA 120

DB 79 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTGAGGGACAGA 138

OY 121 GTACCATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180

DB 139 GTACCATCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 198

OY 181 AAACCAAGAAAGGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGAAGTGGGGTC 240

DB 199 AAACCAAGAAAGGCTCTTAAGCTCTGATCTATGTTGATCCAGTTTGAAGTGGGGTC 258

OY 241 CCATCAAGTTTCAAGCGGAGTGATCTGGGACAGAGTACTCTACCGTCAGACGCTG 300

DB 259 CCATCAAGTTTCAAGCGGAGTGATCTGGGACAGAGTACTCTACCGTCAGACGCTG 318

OY 301 CAGCTCAAGATTTTGGCGATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 360

DB 319 CAGCTCAAGATTTTGGCGATTTACTGTTACTGTTACTGTTACTGTTACTGTTACTG 378

OY 361 GGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 387

DB 379 GGCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 405

RESULT 5

LOCUS BG756818 886 bp mRNA linear EST 15-MAY-2001

DEFINITION 602710291F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4650686 5',

ACCESSION BG756818

VERSION BG756818.1 GI:14067471

KEYWORDS

SOURCE

ORGANISM

human

Homo sapiens

REFERENCE 1 (bases 1 to 886)  
 Mammalia: Euthera; Primates; Catarrhini; Hominiidae; Homo.  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCMI692 row: e column: 23  
 High quality sequence stop: 864.  
 Location/Qualifiers  
 1..886

FEATURES  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:485086"  
 /clone\_1lb="NIH\_MGC\_48"  
 /tissue\_type="primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

BASE COUNT 211 a 258 c 219 g 197 t 1 others  
 ORIGIN

Query Match 85.1%; Score 329.4; DB 10; Length 886;  
 Best Local Similarity 90.7%; Pred. No. 1.2e-89;  
 Matches 351; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGGTGCC 60  
 10 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGGTGCC 69  
 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGAGGAGACA 120  
 70 AGGTGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGAGGAGACA 129  
 121 GTACCATCTGTCAGAGGGAAGTCAAGATTAAGTATTAAATTTGGTATCAGCAG 180  
 130 GTACCATCTGTCAGAGGGAAGTCAAGATTAAGTATTAAATTTGGTATCAGCAG 189  
 181 AAACCAAGAAAGCTCTTAAGTCTCGATATATGTTGATCCAGTTGCAAGGGGGTC 240  
 190 AAACCAAGAAAGCTCTTAAGTCTCGATATTAAGTCTGATCCAGTTGCAAGGGGGTC 249  
 241 CCATCAAGGTTTCAGCGGAGTGTGATCTGGGACAGAAATTCACATCAGCAGCTG 300  
 250 CCATCAAGGTTTCAGCGGAGTGTGATCTGGGACAGAAATTCACATCAGCAGCTG 309  
 301 CAGCTGAAGATTTTGCAGATTAATCTGTCTACAGTTTATAGTACCCCTCGAGCTTC 360  
 310 CAGCTGAAGATTTTGCAGATTAATCTGTCTACAGATTAATAGTACCCGTCACACTTT 369  
 361 GGCCAGGAGCAAGGTGGAATCAAA 387  
 370 GGCTGGGAGCAAGCTGGAGATCAAA 396

RESULT 6  
 BG548281

LOCUS BG548281 864 bp mRNA linear EST 04-APR-2001  
 DEFINITION 602575248F1 NIH\_MGC\_77 Homo sapiens CDNA clone IMAGE:4703483 5',  
 mRNA sequence.  
 ACCESSION BG548281  
 VERSION BG548281.1 GI:13546946  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 864)  
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: CLONTECH Laboratories, Inc.  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLCMI541 row: p column: 12  
 High quality sequence stop: 726.  
 Location/Qualifiers  
 1..864

FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4703483"  
 /clone\_1lb="NIH\_MGC\_77"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggccgctcgcc); Site\_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

BASE COUNT 215 a 253 c 209 g 187 t

ORIGIN

Query Match 84.7%; Score 327.8; DB 10; Length 864;  
 Best Local Similarity 90.4%; Pred. No. 3.6e-89;  
 Matches 350; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

1 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGGTGCC 60  
 27 ATGACATGAGGGTCCCGCTCAGCTCTGGGGCTCTTGGCTGCTGGCCCGAGGTGCC 86  
 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGAGGAGACA 120  
 87 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGAGGAGACA 146  
 121 GTACCATCTGTCAGAGGGAAGTCAAGATTAAGTATTAAATTTGGTATCAGCAG 180  
 147 GTACCATCTGTCAGAGGGAAGTCAAGATTAAGTATTAAATTTGGTATCAGCAG 206  
 181 AAACCAAGAAAGCTCTTAAGTCTCGATATATGTTGATCCAGTTGCAAGGGGGTC 240  
 207 AAACCAAGAAAGCTCTTAAGTCTCGATATTAAGTCTGATCCAGTTGCAAGGGGGTC 266  
 241 CCATCAAGGTTTCAGCGGAGTGTGATCTGGGACAGAAATTCACATCAGCAGCTG 300  
 267 CCATCAAGGTTTCAGCGGAGTGTGATCTGGGACAGAAATTCACATCAGCAGCTG 326  
 301 CAGCTGAAGATTTTGCAGATTAATCTGTCTACAGTTTATAGTACCCCTCGAGCTTC 360  
 327 CAACCTGAAGATTTTGCAGATTAATCTGTCTACAGAGGTTTACACTACACCGCTCACTTTC 386

RESULT	7	391 bp	mRNA	linear	EST 16-FEB-2000
LOCUS	AM404992				
DEFINITION	UT-HF-BLO-abx-a-03-0-UT.1 NIH_MGC_37				
ACCESSION	AM404992				
VERSION	AM404992.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 391)				
TITLE	NIH-MGC http://mgs.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-remail.nih.gov				
	Eco RI site shown at the beginning of the sequence.				
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.				
	cDNA Library Preparation: M.B. Soares Lab				
	cDNA Library Arrayed by: M.B. Soares Lab				
	DNA Sequencing by: M.B. Soares Lab				
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html				
	Seq primer: M13 Forward.				
FEATURES	Location/Qualifiers				
source	1..391				
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	/clone_1lb="NIH.MGC.37"				
	/tissue_type="lymph"				
	/cell_type="germinal center B cells"				
	/cell_line="MGC85"				
	/lab_host="DH10B (LTI)"				
	/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI; constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."				
BASE COUNT	98 a 108 c 94 g 91 t				
ORIGIN					
Query Match	84.4%	Score 326.6	DB 9	Length 391	
Best Local Similarity	91.1%	Pred. No. 5.9e-89			
Matches 347; Conservative 0; Mismatches 34; Indels 0; Gaps 0;					
7	ATGAGGGTCCCGGCGAGCTCTGGGGGCGCTGTGCTGTGGCTCCCGAGGTCCAGATGT	66			
5	AGGAGGGTCCCGGCGAGCTCTGGGGGCGCTGTGCTGTGGCTCCCGAGGTCCAGATGT	64			
67	GACATCCAGATGACCCAGCTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGATCAC	126			
65	GACATCCAGATGACCCAGCTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGATCAC	124			
127	ATCATTGTCAGGGGCAAGTCAGCATTAGATTTATTTAATTGGTATTCAGCAGAAACCA	186			
125	ATCATTGTCAGGGGCAAGTCAGCATTAGATTTATTTAATTGGTATTCAGCAGAAACCA	184			
187	GGAAAGGTCCTCAACCTCTGTATGTATGTGTGATTCAGAGTTTSCAAAGTGGGTCCATCA	246			
185	GGAAAGGTCCTCAACCTCTGTATGTATGTGTGATTCAGAGTTTSCAAAGTGGGTCCATCA	244			
247	AGGTTTCAGGGGCAAGTCAGCATTAGATTTATTTAATTGGTATTCAGCAGAAACCA	306			

Db	245	AGGTTTCATGTGCAGAGCATCTGGGACAGATTTCACTCTCACCATCAGACGTCCTAACCT	304
OY	307	GAAGATTTTGGCACTATTACTGTCTACAGAGTTTATACCCTCGGACGCTTGGCCAA	366
Db	305	GAAGATTTTGGCAATTTACTACTGTCTACGACGAGATTAACAGTATCCCTCTCACTGTGGCCAA	364
OY	367	GGGACACAGGTGGAATCAAA	387
Db	365	GGGACACAGGTGGAATCAAA	385
RESULT	8		
AM383563		453 bp	RNA linear
LOCUS	PM4-HT0348-261199-001-A07	HT0348	Homo sapiens CDNA, mRNA sequence.
ACCESSION	AM383563		
VERSION	AM383563.1	GI:6888131	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 453)		
JOURNAL	HCSP <a href="http://www.ludwig.org.br/ORESTS">http://www.ludwig.org.br/ORESTS</a> .		
COMMENT	The FAPESP/LICR Human Cancer Genome Project Unpublished (1999) Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: <a href="mailto:asimpson@ludwig.org.br">asimpson@ludwig.org.br</a> This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL. ( <a href="http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&amp;t2=PM4-HT0348-261199-001-A07&amp;t3=1999-11-26&amp;t4=1">http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&amp;t2=PM4-HT0348-261199-001-A07&amp;t3=1999-11-26&amp;t4=1</a> ) Seq primer: puc 18 forward High quality sequence stop: 452.		
FEATURES	Location/Qualifiers		
source	1..453		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_lib="HT0348"		
	/dev_stage="Adult"		
	/note="Organ: head,neck; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTS PCR (U.S. letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
BASE COUNT	108 a 125 c 107 g 113 t		
ORIGIN			
Query Match	84.3%;	Score 326.2;	DB 9; Length 453;
Best Local Similarity	90.2%;	Pred. No. 8.3e-89;	
Matches 349;	Conservative 0;	Mismatches 38;	Indels 0; Gaps 0;
OY	1	ATGACATGAGGGGTCCCGCTCAGTCTCTGGGGCTCTTCTGCTGTGGCTCCAGAGTCC	60
Db	5	ATGGACATGAGGGGTCTCTCTCAGCTCTCTGGGGCTCTCTGATCTGGGCTCCGTGGTCC	64
OY	61	AGATTTGACATTCACAGATACCCAGCTCTCATCTTCCCTGCTGCACTGTAGAGGACAGA	120
Db	65	AGATTTGACATTCACATATACCCAGCTCTCATCTTCCCTGCTGCACTTTAGAGACAGA	124
OY	121	GTCACCATCTACTGCGAGGCAAGTCAGACATTAAGTATTAATTAATTTGGTATCAGAG	180
Db	125	GTTACCATCTACTGCGCGGCAAGTCAGACATTAAGTATTAATTAATTTGGTATCAGAG	184

Query Match	Best Local Similarity	Score	DB	Length
Matches 348: Conservative 0; Mismatches 39; Indels 0; Gaps 0;	83.9%;	324.6;	DB 9;	Length 447;
1 ATGCATGAGAGGATCCCGCTCAGCTCCTCGGGGCTCTTCTGCTCTGGCTCCAGAGTCC 60	17 ATGCATGAGAGGATCCCGCTCAGCTCCTCGGGGCTCTTCTGCTCTGGCTCCAGAGTCC 76			
1 AGATGTGACATCCAGATACCCAGTCTTCATCTTCCTGTGTCGATCTGTAGGGGACAGA 120				

Db	77	AGATGGACATCCAGATGACCAGTCTCATCCTCCCTGTCTTGATCTGTAGAGACAGA	136
Oy	121	GTCACCACTACTTGCAGGGCAAGTACAGACATTAGTATTATTAAATTTGGTATCAGCAG	180
Db	137	GTCACCACTACTTGGCGGGCAAGTCAGAGCACTATACAGCTATTTAATTTGATACGACG	196
Oy	181	AACACAGAAAAAGTCTCTAAGCTCTGTATCTATTTGTCATCCAGTTTGGCAAGTGGGTC	240
Db	197	AGACCAAGGAAAAGCCCCCTTAGCTCTCTGATCTATGTGTCATCCAGTTTGCAGAGTGGGTC	256
Oy	241	CCATCAAGTTTCAGCGCAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGACGCTG	300
Db	257	CCATCAAGTTTCAGTGGCAGTGGATCTGGGACAGATTTTCACTCTCACCGTCAGACGCTG	316
Oy	301	CAGCCTGAAGATTTTGGCAGCTTATACGTCTACAGGTTTATAGTACCCCTCGGACGTTG	360
Db	317	CAACCTGAAGATTTTGGCACTTACTCTCTCAACAGAGCTACAGTACCCCGTACAGTTTT	376
Oy	361	GGCCAAGGACCCAGAGTGGAAATCAA	387
Db	377	GGCCAAGGACCCAGAGTGGAAATCAA	403
RESULT	10		
BGS41198	BGS41198	669 bp	mRNA linear EST 03-APR-2001
LOCUS	602569397BP1 NIH_MGC_77	Homo sapiens	cDNA clone IMAGE:4694539 5'
DEFINITION	mRNA sequence.		
ACCESSION	BGS41198		
VERSION	BGS41198.1	GI:13535431	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cga@bsf-research.nhl.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LCM1518 row: k column: 20 High quality sequence stop: 658. Location/Qualifiers 1..669 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4694539" /clone_lib="NIH_MGC_77" /lab_host="DH10B (TI phage-resistant)" /note="Organ: lung; Vector: pMNr-LIB (Clontech); Site: 1; SfiI (ggcgccctcgccg); Site:2: SfiI (ggccattagcc); 5' adaptor 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCGCGCGCATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."		
FEATURES	Source		
BASE COUNT	177 a	189 c	164 g 139 t
ORIGIN			
Query Match	83.1%	Score 321.6;	DB 10; Length 669;





/tissue-type="primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

BASE COUNT 238 a 265 c 241 g 199 t

ORIGIN

Query Match 83.0%; Score 321.4; DB 10; Length 943;  
 Best Local Similarity 89.4%; Pred. No. 3.4e-87;  
 Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

1 ATGACATGAGGATCCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGAGTCC 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 18 ATGACATGAGGATCCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGAGTCC 77

61 AGATGTGACATCCAGATGATGATCCATCTCCCTGCTGATGATGAGGACAGA 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 78 AGATGTGACATCCAGATGATGATCCATCTCCCTGCTGATGATGAGGACAGA 137

121 GTACCATCATTGTCAGAGGCAAGTACAGATATTTAAATGGTATACAGAG 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 138 GTACCATCATTGTCAGAGGCAAGTACAGATATTTAAATGGTATACAGAG 197

181 AAACGAGAAAGCTCTAGCTCTGATCTATGTTGATCCAGTTGGCAAGTGGGTC 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 198 AAACGAGAAAGCTCTAGCTCTGATCTATGTTGATCCAGTTGGCAAGTGGGTC 257

241 CCATCAAGGTTTCAGCGGAGTGTGAGCAGAGTTCACTCTCAGCGTACAGCCTG 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 258 CCATCAAGGTTTCAGCGGAGTGTGAGCAGAGTTCACTCTCAGCGTACAGCCTG 317

301 CAGCTTAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCTCGAGCTTC 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 318 CAGCTTAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCTCGAGCTTC 377

361 GGCCAGGAGCAAGGTGGAATCAAA 387  
 ||||||||||||||||||||||||||||  
 378 GGCCAGGAGCAAGGTGGAATCAAA 404

RESULT 13  
 BF663472 1100 bp mRNA linear EST 21-DEC-2000  
 LOCUS 602144635F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4297736 5',  
 mRNA sequence.  
 VERSION BF663472  
 KEYWORDS BF663472.1 GI:11937367  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1100)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Louis M. Straudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: L10M152 row: f column: 09  
 High quality sequence stop: 704.  
 Location/Qualifiers  
 1..1100  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4297736"  
 /clone\_id="NIH\_MGC\_48"  
 /tissue-type="primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;  
 Site\_2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCAGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

BASE COUNT 283 a 308 c 270 g 239 t

ORIGIN

Query Match 83.0%; Score 321.4; DB 10; Length 1100;  
 Best Local Similarity 89.4%; Pred. No. 3.7e-87;  
 Matches 346; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

1 ATGACATGAGGATCCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGAGTCC 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 8 ATGACATGAGGATCCCGCTCAGCTCTGGGCTCTTCTGCTGCTGCCAGAGTCC 67

61 AGATGTGACATCCAGATGATGATCCATCTCCCTGCTGATGATGAGGACAGA 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 68 AGATGTGACATCCAGATGATGATCCATCTCCCTGCTGATGATGAGGACAGA 127

121 GTACCATCATTGTCAGAGGCAAGTACAGATATTTAAATGGTATACAGAG 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 128 GTACCATCATTGTCAGAGGCAAGTACAGATATTTAAATGGTATACAGAG 187

181 AAACGAGAAAGCTCTAGCTCTGATCTATGTTGATCCAGTTGGCAAGTGGGTC 240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 188 AAACGAGAAAGCTCTAGCTCTGATCTATGTTGATCCAGTTGGCAAGTGGGTC 247

241 CCATCAAGGTTTCAGCGGAGTGTGAGCAGAGTTCACTCTCAGCGTACAGCCTG 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 248 CCATCAAGGTTTCAGCGGAGTGTGAGCAGAGTTCACTCTCAGCGTACAGCCTG 307

301 CAGCTTAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCTCGAGCTTC 360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 308 CAGCTTAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCTCGAGCTTC 367

361 GGCCAGGAGCAAGGTGGAATCAAA 387  
 ||||||||||||||||||||||||||||  
 368 GGCCAGGAGCAAGGTGGAATCAAA 394

RESULT 14  
 BG538665 712 bp mRNA linear EST 03-APR-2001  
 LOCUS 602566902F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4691280 5',  
 mRNA sequence.  
 VERSION BG538665  
 KEYWORDS BG538665.1 GI:13530898  
 EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 712)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.



Search completed: September 23, 2002, 17:06:57  
Job time: 4516 sec

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GenCore, version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:58:42 ; Search time 488.47 Seconds

(without alignments)  
1360.259 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387  
Sequence: 1 ATGCACATGAGGTCGCCG.....GACCAAGGTGAATCAAA 387

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database :  
1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
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6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
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22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	387	100.0	387	19 AAV33309	Anti-human CD23 5E
2	387	100.0	19035	19 AAV61794	Traget Plasmid Man
3	342.2	88.4	729	21 AAA11630	Human immunoglobul
4	334.2	86.4	396	18 AAT75423	Human anti-tumour
5	334.2	86.4	438	22 AAA41157	Human coding sequen
6	329.4	85.1	974	24 AA599473	Anti-human Aflim m
7	326.2	84.3	714	21 AAA46899	DNA encoding the k
8	324.6	83.9	387	21 AA339327	Nucleotide sequenc
9	321.4	83.0	390	21 AA239340	Nucleotide sequenc

10	318.2	82.2	388	18 AAT73441	Human immunoglobul
11	318.2	82.2	388	19 AAV39239	Functional kappa t
12	318.2	82.2	388	20 AA21993	Partial nucleotide
13	318	82.2	936	21 AAA27390	Human IGFM-10 imm
14	316.6	81.8	817	21 AAA27389	Human IGFM-9 immu
15	316.6	81.8	1066	14 AAQ49943	Human anti-HBS 119
16	316.4	81.8	917	21 AA27381	Human IGFM-1 immu
17	311.8	80.6	944	22 AA44892	Human breast cance
18	309.8	80.1	384	21 AA39320	Nucleotide sequenc
19	307.7	79.3	387	16 AA82749	93K9 anti-Varicel
20	307	79.3	409	19 AAV39241	Functional kappa t
21	307	79.3	439	18 AAT73443	Human immunoglobul
22	306	79.1	387	21 AA39325	Nucleotide sequenc
23	305.4	78.9	439	20 AA21995	Partial nucleotide
24	304.2	78.6	705	18 AAT61240	Human anti-RSV mon
25	303.8	78.5	389	15 AA067194	Humanized 1308F VL
26	303.8	78.5	389	17 AAT16181	Hu1308 VL encoding
27	303.6	78.4	928	21 AA27393	Human IGFM-13 imm
28	302.4	78.1	372	21 AA39326	Nucleotide sequenc
29	302	78.0	420	18 AAT73445	Human immunoglobul
30	302	78.0	420	19 AAV39293	Synthetic kappa 11
31	302	78.0	420	20 AA22047	Nucleotide sequenc
32	302	78.0	3819	18 AAT78825	Kappa light chain
33	302	78.0	3819	19 AAV39266	Plasmid pIC65 nuc
34	302	78.0	3819	20 AA22020	Nucleotide sequenc
35	297.8	77.0	384	21 AA39339	Nucleotide sequenc
36	297.4	76.8	390	16 AA087237	Anti-Interleukin-1
37	297	76.7	366	18 AAT79921	Immunoglobulin rB6
38	296.8	76.7	363	23 AAT76095	DNA encoding novel
39	296.8	76.7	702	14 AAQ43773	Sequence encoding
40	296.2	76.5	384	17 AA46133	Monoclonal antibod
41	296.2	76.5	384	18 AAT85844	Monoclonal antibod
42	295	75.8	372	21 AA39322	Nucleotide sequenc
43	293.2	75.8	928	22 AA26799	Human immune respo
44	292.6	75.6	390	21 AA39336	Nucleotide sequenc
45	292.4	75.6	930	22 AAH31350	Human secreted pro

#### ALIGNMENTS

AAV33309	1	AAV33309 standard; DNA: 387 BP.
AAV33309:	18-NOV-1998	(first entry)
DE	Anti-human CD23 5E8 monoclonal antibody light chain variable region DNA.	
XX	Anti-human CD23 5E8 monoclonal antibody: light chain variable region;	
XX	human CD23; IGE: FcεRI/CD23; gamma-1 constant region;	
KW	gamma-3 constant region; allergy; inflammation; autoimmune disease;	
KW	allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.	
XX		
OS	Macaca fascicularis	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..387
FT		/*tag- a
FT		/product= "anti-human CD23 5E8 light chain variable region"
FT		/note= "CDS does not contain a stop codon"
FT	sig-peptide	1..66
FT		/*tag- b
FT	mat-peptide	67..387
FT		/*tag- c
FT	misc-feature	136..168
FT		/*tag- d
FT	/note= "encodes CDR 1 region"	214..234
FT	misc-feature	/*tag- e

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FT      /note= "encodes CDR 2 region"
FT      331..357
FT      /tag= f
FT      /note= "encodes CDR 3 region"
PN      WO9837099-A1.
XX      27-AUG-1998.
XX      17-FEB-1998; 98WO-US02253.
XX      05-FEB-1998; 98US-0803085.
XX      20-FEB-1997; 97US-0803085.
PA      (IDEC-) IDEC PHARM CORP.
PA      (SECK ) SEIRAGAKU CORP.
XX      Kioetzer WS, Nakamura T, Reif ME;
XX      WPI; 1998-467495/40.
DR      P-PsDB; AAW70379.
XX      New anti-human CD23 monoclonal antibody - used for inhibiting Ige
PT      expression to treat or prevent allergic, inflammatory and
PT      auto-immune conditions
XX      Example 1; Pages 106-108; 146pp; English.
XX      The present sequence represents a DNA sequence encoding the light
CC      chain variable region of primate monoclonal antibody anti-human CD23 5F8.
CC      The invention provides primate monoclonal antibodies which specifically
CC      bind human CD23, the low affinity receptor for Ige (FcεRI/CD23),
CC      and comprise either of a human gamma-1 or human gamma-3 constant region
CC      that binds to human Fc gamma receptors and inhibits Ige expression.
CC      The monoclonal antibodies of the invention are claimed to be useful
CC      for inhibiting induced Ige production for treating or preventing
CC      allergic, inflammatory and auto-immune conditions e.g. allergic rhinitis
CC      conjunctivitis, autoimmune haemolytic anaemia, etc.
XX      Sequence 387 BP; 92 A; 102 C; 98 G; 95 T; 0 other:
SQ

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RESULT      2
ID      AAV61794 standard; DNA: 19035 BP.
XX      AAV61794;
XX      07-JUN-1999 (first entry)
DE      Target plasmid Mandy containing anti-CD23 gene.
XX      Mandy; target plasmid; gene integration; gene amplification;
XX      homologous recombination; vector; neomycin phosphotransferase;
XX      neo gene; selectable marker; immunoglobulin; CD23; 5E8; human; ss.
XX      Chimeric - Mus sp.
OS      Chimeric - Escherichia coli.
OS      Chimeric - Baculovirus.
OS      Chimeric - Cytomegalovirus.
OS      Chimeric - Rhesus macaque polyoma virus.
OS      Chimeric - Photinus sp.
OS      Chimeric - Salmonella typhimurium.
XX      Chimeric - Homo sapiens.
XX      Key
FH      Location/Qualifiers
FT      361
FT      misc-feature
FT      /tag=
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering
FT      in the
FT      specification for this sequence"
FT      721
FT      /tag=
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering
FT      in the
FT      specification for this sequence"
FT      2941
FT      /tag=
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering
FT      in the
FT      specification for this sequence"
FT      3301
FT      /tag=
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering
FT      in the
FT      specification for this sequence"
FT      misc-feature
FT      4261
FT      /tag=
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to
FT      maintain the nucleotide numbering
FT      in the
FT      specification for this sequence"
FT      4621..4622
FT      /tag=
FT      /note= "these bases represent nucleotides missing
FT      from the sequence given in the
FT      specification. They are included to
FT      maintain the nucleotide numbering in the
FT      specification for this sequence"
FT      misc-feature
FT      8161
FT      /tag=
FT      /note= "this base represents a nucleotide missing
FT      from the sequence given in the
FT      specification. It is included to

```

[illegible]

XX	Site specific integration of DNA in mammals for expressing, e.g.
PT	immunoglobulins - comprises homologous recombination using
PT	selectable marker and target plasmids.
XX	
PS	Example 1; Fig 10; 114pp; English.
XX	This is the nucleotide sequence of novel target plasmid Mandy.
CC	The plasmid includes an inactivated murine dihydrofolate reductase
CC	(DHFR) gene, the Escherichia coli beta-galactosidase gene,
CC	baculovirus DNA, a cassette comprising the promoter and enhancer
CC	elements from cytomegalovirus and SV40 virus, the E. coli
CC	beta-glucuronidase (Gus) gene, firefly luciferase gene, an
CC	inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)
CC	gene and transposon Tns neomycin phosphotransferase (neo) gene
CC	sequences. In a pBR-derived backbone, and also an anti-human CD23
CC	IGF receptor human gamma-1 monoclonal antibody 5E8 gene. The
CC	invention provides a novel method for integrating a desired
CC	exogenous DNA at a target site within the genome of a mammalian
CC	cell via homologous recombination. This involves transfecting the
CC	cell with a 'marker plasmid' such as Desmond (see AAV61792), which
CC	contains a unique sequence that is foreign to the mammalian cell
CC	genome and which provides a substrate for homologous recombination,
CC	followed by transfection with a 'target plasmid', such as Mandy
CC	or Molly (see AAV61793), containing a sequence which provides for
CC	homologous recombination with the unique sequences contained in
CC	the marker plasmid, and further comprising a desired DNA that is
CC	to be integrated into the mammalian cells, typically an
CC	immunoglobulin or other secreted mammalian glycoprotein. The
CC	homologous recombination system utilises the neo gene as a
CC	dominant selectable marker. The neo gene is split into 3 exons.
CC	Exon 3 is present on the marker plasmid and becomes integrated
CC	into the host cell genome upon integration of the marker plasmid
CC	into the mammalian cells. Exons 1 and 2 are present on the
CC	targeting plasmid, and are separated by an intron into which at
CC	least one gene of interest is cloned. Homologous recombination
CC	of the targeting vector with the integrated marking vector results
CC	in correct splicing of all 3 exons of the neo gene and expression
CC	of a functional neo protein. The method is applicable to all
CC	mammalian cells, and can be used to express any type of recombinant
CC	protein. The use of a triply spliced selectable marker means that
CC	all selected colonies arise from homologous recombination. In
CC	addition, the number of colonies that need to be screened to
CC	identify high producer clones is reduced. An amplifiable gene can
CC	be inserted on integration of the marking vector, so that when a
CC	gene is targeted to this site, the gene is further enhanced by gene
CC	amplification.
XX	
XX	Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other:
S0	
XX	Query Match 100.0%; Score 387; DB 19; Length 19035;
XX	Best Local Similarity 100.0%; Pred. No. 3.9e-108;
XX	Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	1 ATGCACATGAGGGTCCCGCTCAGCTCCTCGGGGCTCTTCTGCTCGCTCCAGGTGCC 60
DB	7541 atgagcatgagggtcccgctcagctcctcggggtccctctcgtcgtcccaagtgc 7600
QY	61 AGATGTGACATTCAGATGACCCAGTCTTCATCTTCCCTGTCTGCATCTGTAGGGACAGA 120
DB	7601 agatgtgacatccagatgacccagctccatctccctcgtcgtcatctgtaagggacaga 7660
QY	121 GTCACATTCACCTGTCAGGGGCAAGTCAGGACATAGTATTAATTAAATGGTATCAGCG 180
DB	7661 gtcacatcactctgaaggcaagtcaggaacatlaagtatattaaatggtatcagcgg 7720
QY	181 AAACGAGAAAAAGCTCTTAAGCTCTGATCTTATGTGGTCATCCAGTTGCAAGAGTGGGATC 240
DB	7721 aaacgagaaaaagctcctaagctcctgatcatatgttgcattcagtttgaagaagtgggttc 7780
QY	241 CCATCAAGGTTTCAGGGGAGTGGATCTTGGGACAGAGATTCTACCTCACCCTCAGACGCTGC 300

Db 7781 ccatcaaggtcagcgagtgatctgagacagatctactccagctcagcgctg 7840  
 QY 301 CAGCCGAGGATTTCGAGCTTATTCGTACAGGTTATAGTACCCCTGGAGCTTC 360  
 Db 7841 cagccgaagatttgcagctactactgtctacaggttactagctccctcgagcttc 7900  
 QY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387  
 Db 7901 ggccaagagccaaggtggaatcaaa 7927

RESULT 3  
 AA11630  
 ID AA11630 standard; DNA; 729 BP.  
 AC AA11630;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Human immunoglobulin light chain kappa region subgroup type I DNA.  
 XX  
 KW Fas; antibody: human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antineumatic; anti-Fas;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;  
 KW multiple sclerosis; Basedow's disease; myasthenia gravis;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomypathy; glomerulonephritis; hepatitis; transplant rejection; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI: 2000-258930/23.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 XX Example 2; Page 154; 263pp; English.

CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a human immunoglobulin light chain kappa variable region subgroup type I  
 CC which is used in the construction of humanised anti-Fas antibody  
 CC constructs described in the method of the invention.  
 XX  
 XX Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;  
 XX

Query Match 88.4%; Score 342.2; DB 21; Length 729;  
 Best Local Similarity 92.8%; Pred No. 6e-95;  
 Matches 359; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGATCCCGCTCAGCTCTGGGGCTCTCTGCTGCTCCAGGTGCC 60  
 Db 7 atgacatgagggtcccgctcagctctgctcgggctctctgctcaggtgcc 66  
 QY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTCTGCAATCTAGGAGACAGA 120  
 Db 67 agatgtgacatccagatgacccaagctccatccctctgcatctgaggaagacaga 126  
 QY 121 GTACCATCATCTTCGAGGCAAGTCAGACATTAGGTATTTAAATGGTATCAGCAG 180  
 Db 127 gtaccatcatcttcgagggcaagtcagagcatatagaagctatctaattgatacagcg 186  
 QY 181 AAACGAGAAAGCTCTTAAGCTCTGATCTATGTGTGATCCAGTTGCAAAAGTGGGTC 240  
 Db 187 aaaccgaggaagagcccccctaagctccgatactatgctgcagctcagttgaaagtgggttc 246  
 QY 241 CCATCAAGTTCAGCGGCGAGTGGATCTGGAGACAGATTACGTCCAGCTCAGCACCTCG 300  
 Db 247 ccatcaaggtcagtgagcgatgacatcggagacagattcaaccatccatcagcagctcg 306  
 QY 301 CAGCCTGAAGATTTCGAGCTTATTCGTACAGGTTATAGTACCCCTGGAGCTTC 360  
 Db 307 caacctgaagatttgcagctactactgtctacacagagtacagctccctcgagcttc 366  
 QY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387  
 Db 367 ggccaagagccaaggtggaatcaaa 393

RESULT 4  
 AAT75423  
 ID AAT75423 standard; cDNA; 396 BP.  
 XX  
 AC AAT75423;  
 XX  
 DT 12-SEP-1997 (first entry)  
 XX  
 DE Human anti-tumour antigen antibody light chain variable region cDNA.  
 XX  
 KW Human: tumour antigen; cancer; monoclonal; antibody; light chain;  
 KW variable region; medicine; pharmacology; biochemistry; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..66 /\*tag= a  
 FT mat\_peptide 67..396 /\*tag= b  
 FT  
 XX JP09100300-A.  
 XX 15-APR-1997.  
 PD  
 XX





12-MAR-2002 (first entry)

Anti-human AILM monoclonal antibody clone Unab-136, light chain cDNA.

Human; antirheumatic; antiarthritis; antidiabetic; antipsoriatic; antiallergic; anticancer; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; AILM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; ss; graft versus host reaction; immune rejection; intestinal immunity; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.

Homo sapiens.

WO200187981-A2.

22-NOV-2001.

15-MAY-2001; 2001WO-JP04035.

18-MAY-2000; 2000JP-0147116.

30-MAR-2001; 2001JP-0099508.

(NISB ) JAPAN TOBACCO INC.

Tsuji T, Tezuka K, Hori N;

WPI: 2002-075313/10.

P-PSDB; AAU74297.

New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid arthritis, multiple sclerosis and inflammation

Claim 45; Page 267-270; 300pp; English.

The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILM). (I) is useful for modulating signal transduction into a cell mediated by AILM, for modulating proliferation of AILM-expressing cells, for modulating production of a cytokine from AILM-expressing cells, and for inducing antibody-dependent cytotoxicity against AILM-expressing cells and/or immune cytolysis or apoptosis of AILM-expressing cells. (I) is useful for treating, preventing or prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with AILM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammatory dermatosis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, psoriasis, autoimmune or allergic disorders, inflammation, graft versus host reaction, graft versus host disease, immune rejection, disorders caused by abnormal intestinal immunity, specifically inflammatory intestinal disorders such as ulcerative colitis, pneumonia, hepatitis, nephritis, vasculitis, and pancreatitis. (I) induces no serious immunorejection due to antigenicity to human, i.e., human anti-mouse antigenicity (HAM) in a host. AA59444-AA59947 represent anti-human AILM monoclonal antibody coding sequences and PCR primers of the invention.

Sequence 974 BP; 246 A; 282 C; 232 G; 214 T; 0 other;

Query Match	85.1%	Score 329.4	DB 24	Length 974
Best Local Similarity	90.7%	Pred. No. 5,6e-91		
Matches 351; Conservative	0	Mismatches 36;	Indels 0	Gaps 0
1	ATGGACATGAGGGTCCCGCCTCAGCTCCTCGGGGCTTCCTCTGCTGCCAGGTGCC	60		

Dd	39	atggaacatgaggggtccccgcctcaagctcctcgagggtccctcgtcgtctcgtgtgccaggttc	98
Qy	61	AGATGTGCATCATGAGATGACCCAGCTCCTCATCTTCCCTGTGTGCATCTGTAGGGGACAGA	120
Dd	99	agatgtagcacatccagatlgaccacagttcccatcttcglttcgtcgtcattgtagagacaga	158
Qy	121	GTCACCATCACTTTCGAGGGCACAGTGACGAACTTAGGTATTATTATAATTGTGTATCGACG	180
Dd	159	gtccacatcaccttgcgcggagtgcaaggatataagagtlgtltagccgtgatacaga	218
Qy	181	AAACAGGAAAAAGCTCCTTAAGCTTCCTATCTATGTTGCATCCAGTTTGCAAAAGTGGGTC	240
Dd	219	aaacacgggaaaagcccctaactaaccttcgatctatagtgtcacccaagtlttgaaagtgggtc	278
Qy	241	CCATCAAGGTTTCAGCGGCGAGTGTGAGACTGTGGACAGAGTTCACTTCACGCTCAGACCTG	300
Dd	279	ccatcaaggttcagcggcagtgatgtacltgcggacaagattcacctcacatcagcagccgtg	338
Qy	301	CAGCTCAAGATTTTTGGACTTATTACTGTCTACAGTTTATAGTATACCCTGGAGCTTC	360
Dd	339	cagcgttaaagatttgtcaactactatgtcacacaggtcaaacagtlttcccgltgagcgttc	398
Qy	361	GGCCAAGGACCAAGCTGGAATCAAA	387
Dd	399	ggccaaggagaccaagtgtagaatcaaa	425
 RESULT 7 AAAA6899 ID AAAA6899 standard; DNA; 714 BP. XX AC AAAA6899; Dd DT 03-OCF-2000 (first entry) XX DE DNA encoding the kappa chain of immunoglobulin clone 11.2.1. XX KX KW Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection, proliferative disorder; cancer; immunodeficient disorder; ss. KX OS Homo sapiens. XX FH Key Location/Qualifiers FT CDS 67..714 FT CDS /*tag= a XX PN WO200037504-A2. XX PD 29-JUN-2000. XX PF 23-DEC-1999; 99MO-US30895. XX PR 23-DEC-1998; 98US-0113647. XX PA (PEIZ ) PFIZER INC. PA (ABGE-) ABGENIX INC. XX PI Hanson DC, Neveu MJ, Mueller EE, Hanke JH, Gilman SC, Davis CG; PI Corvalan JR; XX DR WPI: 2000-442647/38. DR P-PSDB: AAY93735. XX PT Novel antibodies capable of binding cytotoxic T-lymphocyte antigen CTLA-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders - XX PS Example 2; Fig 22r; 157pp; English.			

CC variable region, comprising a modified contiguous sequence from a  
CC FRI-FR3 sequence encoded by a human VH3-33 family gene. The  
CC modifications are contained in CDR1, CDR2 and/or framework regions.  
CC The antibodies may be used to inhibit CTLA-4 and down-regulate the  
CC immune system to treat hyperimmunity disorders (e.g. autoimmune  
CC disease, diabetes and graft rejection) and proliferative disorders  
CC (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate  
CC immune system to up-regulate immunodeficient disorders.

SQ Sequence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;

Query Match 84.3%; Score 326.2; DB 21; Length 714;  
Best Local Similarity 90.2%; Pred. No. 4.8e-90;  
Matches 349; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 1 ATGGACATGAGGTCCTCCGCTCAGTCTCTGGGCTCTCTGCTGCTGGCTCCAGGTC 60  
DB 1 atggacatgaggtctcccgctcagctcctcctggtgctctgctcgtcgcaggtgccc 60  
OY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGATCTAGGGACAGA 120  
DB 61 agatgtgacatccagatgacccagctccatcctcctgtcgtcagctgtaggagacaga 120  
OY 121 GTCCACCATCTTGCAGGGCAGTGCAGACATTAATTAATTGCTATCAGCAG 180  
DB 121 gtccaccatcttgcagggcagtgacagacattatgattatgctatcagcag 180  
OY 181 AAACGAGAAAGCTCTAAGCTCTGATCTATGTGATCCAGTTTGCAGAGTGAGGTC 240  
DB 181 aaacgagaaagctcttaagctctgattgtgagtcacattatgattatgagtcag 240  
OY 241 CCATCAAGGTTTACGCGGAGTGTGAGACAGTTCACCTCCGACAGCTTC 300  
DB 241 ccatacaagttcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 300  
OY 301 CAGCCTGAGATTGTCGAGTCTTACTGCTCTACAGTTTATAGTACCCCTCGAGCTTC 360  
DB 301 caacctgagaatttgcagcttacttactctgcaacagattatcagctacatcacttc 360  
OY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387  
DB 361 ggccctggagaccaaagtggaatacaaa 387

RESULT 8  
AAZ39327

ID AAZ39327 standard; DNA; 387 BP.

AC AAZ39327;

DT 15-FEB-2000 (first entry)

DE Nucleotide sequence of chimpanzee V kappa CDNA clone 46-14.

KM Complementarity determining region; antibody; primate; immunogenicity;  
KW Old World ape; Old World monkey; antigen-binding affinity; ss.

OS Pan troglodytes.

PN WO9955369-A1.

PD 04-NOV-1999.

PF 28-APR-1999; 99WO-US09131.

PR 28-APR-1998; 98US-0083367.

PA (SMK ) SMITHKLINE BEECHAM CORP.

PI Taylor AH;

DR WPI; 2000-023265/02.

DR P-PSDB; AAY56659, AAY56724.

XX

XX

PT

XX

XX

PS

XX

CC

CC

CC

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CC

Antibodies containing donor complementarity determining regions and  
non-human primate acceptor frameworks, having reduced immunogenicity in  
humans -  
Example 2; Page 67-68; 123pp; English.

The invention provides an antibody (Ab) comprising donor CDRs  
(complementarity determining regions) derived from a non-human antigen-  
specific donor antibody, and an acceptor framework from a non-human  
primate. The Abs are prepared by grafting CDRs from a non-human antigen-  
specific donor antibody onto homologous Old World ape or monkey acceptor  
frameworks. The Abs have reduced immunogenicity and are better tolerated  
in humans (because of the close similarity between the human and primate  
proteins), but retain the full antigen-binding affinity of the donor  
antibody.

SQ Sequence 387 BP; 94 A; 104 C; 95 G; 94 T; 0 other;

Query Match 83.9%; Score 324.6; DB 21; Length 387;  
Best Local Similarity 89.9%; Pred. No. 1.2e-89;  
Matches 348; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY 1 ATGGACATGAGGTCCTCCGCTCAGTCTCTGGGCTCTCTGCTGCTGGCTCCAGGTC 60  
DB 1 atggacatgaggtctcccgctcagctcctcctggtgctctgctcgtcgtcaggtacc 60  
OY 61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGATCTAGGGACAGA 120  
DB 61 agatgtgacatccagatgacccagctccatcctcctgtcgtcagctgtaggagacaga 120  
OY 121 GTCCACCATCTTGCAGGGCAGTGCAGACATTAATTAATTGCTATCAGCAG 180  
DB 121 gtccaccatcttgcagggcagtgacagacattatgattatgctatcagcag 180  
OY 181 AAACGAGAAAGCTCTAAGCTCTGATCTATGTGATCCAGTTTGCAGAGTGAGGTC 240  
DB 181 aaacgagaaagctcttaagctctgattgtgagtcacattatgattatgagtcag 240  
OY 241 CCATCAAGGTTTACGCGGAGTGTGAGACAGTTCACCTCCGACAGCTTC 300  
DB 241 ccatacaagttcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 300  
OY 301 CAGCCTGAGATTGTCGAGTCTTACTGCTCTACAGTTTATAGTACCCCTCGAGCTTC 360  
DB 301 caacctgagaatttgcagcttacttactctgcaacagattatcagctacatcacttc 360  
OY 361 GGCCAAAGGACCAAGGTGGAATCAAA 387  
DB 361 ggccctggagaccaaagtggaatacaaa 387

RESULT 9  
AAZ39340

ID AAZ39340 standard; DNA; 390 BP.

AC AAZ39340;

DT 15-FEB-2000 (first entry)

DE Nucleotide sequence of Cynomolgus V kappa CDNA clone 4-10.

KM Complementarity determining region; antibody; primate; immunogenicity;  
KW Old World ape; Old World monkey; antigen-binding affinity; ss.

OS Macaca cynomolgus.

PN WO9955369-A1.

PD 04-NOV-1999.

DR

[illegible]

KW	Ig; affinity constant; human; antigen: hybridoma; B cell; transgene;
KV	transgenic mouse; CD4 antibody; autoimmune; inflammatory;
KM	transplant rejection; ss.
XX	
OS	Homo sapiens.
PN	M09713852-A1.
PD	17-APR-1997.
PF	10-OCT-1996; 96WO-US16433.
PR	10-OCT-1995; 95US-0544404.
PA	(GENP-) GENPHARM INT INC.
P1	Kay RM, Lonberg N;
DR	WP1: 1997-235888/21.
PT	Novel anti-CD4 antibody produced by transgenic mice used in the treatment of auto-immune disease etc.
PS	Claim 44; Page 255; 396pp; English.
CC	A novel composition has been developed which comprises an immunoglobulin (Ig) having an affinity constant ( $K_a$ ) of at least 2 multiply 10000000 M <sup>-1</sup> for binding to a predetermined human antigen. The present sequence represents a human light chain variable-region partial nucleotide sequence, 10C5 kappa, which encodes an amino acid sequence from a claimed immunoglobulin that specifically binds human CD4. The anti-CD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These antibodies reduce activity of CD4 cells and reduce undesirable autoimmune reactions, inflammatory response and transplant rejection. Transgenic animals are capable of producing heterologous antibodies of multiple isotypes by undergoing isotype switching. These animals produce a first Ig type that is necessary for antigen-stimulated B-cell maturation and can switch to encode and produce one or more subsequent heterologous isotypes.
SQ	Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other:
Query Match	82.2%; Score 318.2; DB 18; Length 388;
Best Local Similarity	88.9%; Pred. No. 1.1e-87;
Matches 344; Conservative	0; Mismatches 43; Indels 0; Gaps 0.
OY	1 ATGGCATGATGAGGGTCCCGGTTCACGCCGCCTTGTTGTCATCTGTAGGGACAGA 120
Dd	1 atggcattgatagttgtcccgcttcaggccccgcgggtcttctgcttgatcccagaagtcc 60
OY	61 AGATTGCAATCCAGATGACCACCAGTCTCCATCTTCCCCTGTGCAATCTGTAGGGACAGA 120
Dd	61 agattgcacatacgaatgaccaccagctcccatctccgtctgcatctgttagagacaga 120
OY	121 GTCACCATCTACTGACAGGGCAAAGTAGACAATTAATTTAAATTTGGTATCAGCAG 180
Dd	121 gtcacctactacttgcacggcgagctcaagatatatacagctggttagcctgttatcacat 180
OY	181 AAACGAGAAAAAGCTCTAAGGCTCTGATCTATGTTGGCATCCAGTTTGAAGAAGTGGGATC 240
Dd	181 aaacgagaaaaagcccttaagctcttgtatctatgtctgtcatccaglttgaaagtgggttc 240
OY	241 CCATCAAGTTTCACGCGAGATGATCTGGGACAGAGTTTCATCTCAGCCGTAGCAGCCTG 300
Dd	241 ccatcaagtgttcacggcagtgatctggacaagattcaactccaaccalcagcagctcy 300
OY	301 CAGCCTGAAGATTTTTGGCAGCTTATNCTGCTCAACAGGTTTANAGNACCCCTGGAGGCTTC 360
Dd	301 cagcctgaagattttggcaacttactatctgtcaaacaggtctaagttgccgttacacttt 360
OY	361 GGCCAAGGGACCAAGGTGAATAATCAA 387

Db	361	g9ccaggggaccagctgagatcaaa	387
RESULT	11		
ID	AAV39239	standard; DNA; 388 BP.	
AC	AAV39239;		
XX	18-DEC-1998	(first entry)	
DE	Functional kappa transcript isolated from transgenic cell line 10C5.		
XX	Transgenic animal; human heterologous antibody; transgene;		
KW	isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;		
KW	autoimmune reaction; inflammatory response; transplant rejection;		
KW	acid induced lung injury; acute adult respiratory distress syndrome;		
KW	ARDS; vasculitis; septic shock; allergic reaction; asthma;		
XX	cystic fibrosis; ss.		
XX	Synthetic.		
OS	Homo sapiens.		
OS	Mus sp.		
PN	W09824884-A1.		
PD	11-JUN-1998.		
PF	01-DEC-1997; 97MO-US21803.		
PR	02-DEC-1996; 96US-0758417.		
PA	(GENP-) GENPHARM INT.		
PI	Kay RM, Lonberg N;		
DR	WPI: 1998-333306/29.		
PT	Hybridoma producing antibody specific for interleukin-8 - used to		
PT	prevent efflux of neutrophils from vasculature, and treat		
PT	reperfusion injury		
XX	Example 41, Page 304; 452pp; English.		
XX	AAV39232-41 represent functional transcripts of a human Igkappa		
CC	anti-CD4 antibody. The sequences are isolated from 5 different		
CC	transgenic mouse hybridoma cell lines. The specification describes		
CC	transgenic non-human animals, especially a mouse, which are capable of		
CC	producing a human heterologous antibodies of multiple isotypes by		
CC	undergoing isotype switching. The transgenic animals have human heavy and		
CC	light chain transgenes. The transgenes are capable of functionally		
CC	rearranging a heterologous diversity (D) gene in a		
CC	variable-diversity-junction (V-D-J) recombination. The transgenes included		
CC	a heavy chain transgene comprising at least one V, D and J gene segment,		
CC	and one constant region gene segment. The immunoglobulin (Ig) light chain		
CC	transgene comprises at least one V and J gene segment and one constant		
CC	region gene segment. The gene segments are heterologous to the transgenic		
CC	animal. The antibody can be used to prevent efflux of neutrophils from		
CC	vasculature. It can also be used to treat reperfusion injury. CD4 binding		
CC	antibodies are used to reduce undesirable autoimmune reactions,		
CC	inflammatory responses and rejection of transplanted organs. The		
CC	anti-IL-8 antibodies can reduce tissue damage and prolong survival in		
CC	animal models of acute adult respiratory distress syndrome (ARDS) and		
CC	acid induced lung injury. The anti-IL-8 antibodies can also be used for		
CC	the treatment of vasculitis, septic shock, allergic reactions (e.g.		
CC	asthma) and cystic fibrosis.		
XX	Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;		
XX			
Query Match	82.2%;	Score 318.2; DB 19;	Length 388;
Best Local Similarity	88.9%;	Pred. No. 1,1e-87;	

Matches	344	Conservative	0	Mismatches	43	Indels	0	Gaps	0
QY	1	ATGGACATGAGGCTCCCGCTCAGCTCCGCGGGGCTCTTCTGCTCGTGGCTCCAGGTGCC	60						
Db	1	atggacatgahgtgtcccgctcagctcccggggtctctgctgctcgtgtcccaagtttc	60						
QY	61	AGATGTGACATCCAGATGACCACCAAGTCCATCTTCCCTGTGCAATCTGTAGGGGACAGA	120						
Db	61	agatgacatcccaatgatacccaagctccatcttcctcgtctgcatactctgtagagacaga	120						
QY	121	GTCCACCATCTCTGCAAGGCGCAAGTACAGACATTAGTATTATTAAATTGGTATACGCG	180						
Db	121	gtccaccatcactctgcggtcgagatcaagataatgaacagctgtgtagccggtatcagct	180						
QY	181	AAACGAGGAAAAGCTCCCTAAGCTCCGATCTATGTGTCATCTCCAGTTTGCAAGTGGGGGTC	240						
Db	181	aaacccagggaaagcccccctaagctccctgacatctatgtctgcaccagttgcaaaagtggggc	240						
QY	241	CCATCAAGGTTTAGCGCGCATGTGATCTGGGACAGAGTTACTCTCACTCCAGCCGTACGACCCG	300						
Db	241	ccatcaaggttcacgagcgagctgagctctggagacagatttcacctccacatacgaacgacgtg	300						
QY	301	CAGCCTGAAGATTTTGGCGACTTATTACTGTCTACAGGTTATAGTACCCTCGGAGGTC	360						
Db	301	cagcctgaagaattcttgcacacttactatctgtcaacagcctaataagttctcccgtaacacttt	360						
QY	361	GGCCAAGGACCACGATGGGAATCAAA	387						
Db	361	ggccaggagggaccacgctgagatcaaa	387						

```

RESULT 12
ID AAZ21993
XX AAZ21993 standard; DNA; 388 BP.
AC AAZ21993;
DT 24-NOV-1999 (first entry)
DE Partial nucleotide sequence for a functional transcript 10C5-kappa.
XX
XX Transgenic animal; heterologous antibody; hybridoma; B cell;
KW transgenic mouse; human heavy chain transgene; diroxin; PCR primer;
KW human light chain transgene; immortalized cell; immunoglobulin;
KW Shiga-like toxin; autoimmune disease; cancer; infectious disease;
KW transplant rejection; blood disorder; coagulation disorder; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO945962-A1.
PN 16-SEP-1999.
XX
XX 12-MAR-1999; 99WO-US05535.
PD
XX
XX 13-MAR-1998; 98US-0042353.
XX
XX (GENP-) GENPHARM INT INC.
PA
XX
XX Lonberg N, Fishwild DM, Ball WJ;
XX
XX WPI; 1999-551219/46.
XX
XX Novel transgenic non-human animals used to produce heterologous
PT antibodies
PT
XX
XX Example 41; Page 305; 484pp; English.
XX
XX The specification describes transgenic animals that are capable of
CC producing a heterologous antibody. The antibodies are isolated from a
CC hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC having a genome comprising a human heavy chain transgene and a human

```

CC light chain transgene. The B cells are fused to immortalized cells  
CC suitable for generating a hybridoma, which produces a detectable  
CC amount of an immunoglobulin that specifically binds dioxin or  
CC Shiga-like toxin. B cells from transgenic animals can be used to  
CC generate hybridomas expressing monoclonal high affinity human sequence  
CC antibodies. Antibodies produced from the transgenic animals of the  
CC invention can be used to treat human diseases, e.g. autoimmune  
CC diseases, cancer, infectious disease, transplant rejection, blood  
CC disorders such as coagulation disorders and other diseases. The  
CC present sequence represents a partial nucleotide sequence for a  
CC functional transcript used in the course of the invention.  
XX  
XX  
SQ Sequence 388 BP; 89 A; 107 C; 97 G; 95 T; 0 other;

Query Match 82.2%; Score 318.2; DB 20; Length 388;  
Best Local Similarity 88.9%; Pred. No. 1.1e-87;  
Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTGCGGCTCTTGTGCTGCTCCAGGTGCC 60  
DB 1 atggacatgaggtcccgctcagctcttggtgctctgctcgttccaggtcc 60  
QY 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGTGCTGCTAGGGAGAGA 120  
DB 61 agatgtgacatccagatgacccagtcctcctcgttgcgtatctgtagagagaga 120  
QY 121 GTGACCATCACTTGACGAGCAAGTACAGACATTAAGTATTAAATTTGATACAGAG 180  
DB 121 gtgaccatcacttgctgggagagatagatagacagcgtgttagctgtatcagcat 180  
QY 181 AAACCCAGAAAAGCTCCTTAAGTCTGATATGATGTCATCCAGTTGCAAGTGGGCTC 240  
DB 181 aaacccagaaaagctccttaagtcctgattcatatgctgcatccagttgcaaaagtgggctc 240  
QY 241 CCATCAAGGTTTCAGCGGCAATGATGATGCGAGATGCTCCTACCCGACAGAGCTG 300  
DB 241 ccatacaagttcagcgagcagctgagatcgggacagattcctccaccacacagacgtc 300  
QY 301 CAGCCTGAAGATTTTGGAGATTTACTGTCTACAGATTATAGTACCCCTCGACGCTTC 360  
DB 301 cagcctgaagatttggagatttgaactactatgtgcaacagagctatagttcccgtaacattt 360  
QY 361 GGCCCAAGGACCAAGTGCAGAAATCAAA 387  
DB 361 ggcacagggaccaaagctgagatcaaa 387

RESULT 13

ID AAA27390 standard; cDNA; 936 BP.

AC AAA27390;

DT 16-AUG-2000 (first entry)

DE Human IGFM-10 immunoglobulin coding sequence.

KW Human; immunoglobulin; IGFM-10; IGFM; immune disorder; cancer;

OS Infection; inflammation; haematopoiesis; AIDS; allergy; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX 25-MAY-2000.  
PD 19-NOV-1999; 99MO-US27566.  
XX  
XX  
PF 19-NOV-1998; 99US-0113635.  
PR 19-NOV-1998; 99US-0113635.  
PR 22-DEC-1998; 98US-0113635.  
PR 07-APR-1999; 99US-0128194.  
XX  
XX (INCY-) INCYTE PHARM INC.  
XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;  
PI Lu DM, Lal P, Hillman JL, Tang J;  
XX WPI; 2000-387796/33.  
DR P-PSDB; AAY96298.  
XX  
XX  
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the  
PT protein is useful for preventing and treating disorders associated with  
PT altered levels of the protein such as cancer, immune system disorders  
PT  
PS Claim 9; Page 99-100; 105pp; English.

CC The present sequence is the human immunoglobulin superfamily protein  
CC IGFM-10 gene, which was isolated from a cDNA library of colon  
CC tissue. It is expressed in reproductive, gastrointestinal and  
CC cardiovascular tissue, where cancer and inflammation are common. The  
CC gene, protein, its antibodies, agonists and antagonists are suitable for  
CC diagnosing and treating many diseases, including cancer, immune system  
CC disorders (such as inflammation, AIDS, allergies, anaemia,  
CC arteriosclerosis, asthma, atherosclerosis, cholelithiasis, Crohn's  
CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,  
CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,  
CC systemic lupus erythematosus and ulcerative colitis), complications of  
CC cancer, haemodialysis and extracorporeal circulation, trauma and  
CC haematopoietic cancer (such as leukaemia) and infections caused by  
CC bacteria, viruses, fungi or parasites.  
XX  
XX

SQ Sequence 936 BP; 239 A; 276 C; 214 G; 207 T; 0 other;

Query Match 82.2%; Score 318; DB 21; Length 936;  
Best Local Similarity 90.3%; Pred. No. 1.7e-87;  
Matches 352; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 1 ATGGACATGAGGGTCCCGCTCAGCTCTGCGGCTCTTGTGCTGCTCCAGGTGCC 60  
DB 1 atggacatgaggtcccgctcagctcttggtgctctgctcgttccaggtcc 60  
QY 61 AGATGTGACATCCAGATGACCCAGTCCATCTTCCCTGTGCTGCTAGGGAGAGA 120  
DB 61 agatgtgacatccagatgacccagtcctcctcgttgcgtatctgttagagagaga 120  
QY 121 GTGACCATCACTTGACGAGCAAGTACAGACATTAAGTATTAAATTTGATACAGAG 180  
DB 121 gtgaccatcacttgctgggagagatagatagacagcgtgttagctgtatcagcat 180  
QY 181 AAACCCAGAAAAGCTCCTTAAGTCTGATATGATGTCATCCAGTTGCAAGTGGGCTC 240  
DB 181 aaacccagaaaagctccttaagtcctgattcatatgctgcatccagttgcaaaagtgggctc 240  
QY 241 CCATCAAGGTTTCAGCGGCAATGATGATGCGAGATGCTCCTACCCGACAGAGCTG 300  
DB 241 ccatacaagttcagcgagcagctgagatcgggacagattcctccaccacacagacgtc 300  
QY 301 CAGCCTGAAGATTTTGGAGATTTACTGTCTACAGATTATAGTACCCCTCGG---ACG 357  
DB 301 cagcctgaagatttggagatttgaactactatgtgcaacagagctatagttcccgtaacattt 357  
QY 358 TTGGCCCAAGGACCAAGTGCAGAAATCAAA 387  
DB 358 ttggcccaaggaccaaagctgagatcaaa 387

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RESULT 14
ID AAA27389 standard; cDNA; 817 BP.
XX
AC AAA27389;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-9 immunoglobulin coding sequence.
XX
KW Human; immunoglobulin; IGFAM-9; IGFAM; immune disorder; cancer;
infection; inflammation; haematopoiesis; AIDS; allergy; ss.
XX
OS Homo sapiens.
XX
FH Key 11..721 Location/Qualifiers
FT CDS /tag= a
FT sig_peptide /product= "IGFAM-9"
FT mat_peptide /tag= b
FT /77..718
FT /tag= c
XX
PN WO200029583-A2.
XX
PD 25-MAY-2000.
XX
PF 19-NOV-1999; 99WO-US27566.
XX
PR 19-NOV-1998; 99US-0113635.
PR 22-DEC-1998; 98US-0113635.
PR 07-APR-1999; 99US-0128194.
XX
PA (INCYTE) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI Lu DM, Lai P, Hillman JL, Yang J;
XX
DR WPI: 2000-387796/33.
DR P-PSDB: AAY96297.
XX
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders
PT
XX
PS Claim 9; Page 99; 105pp; English.
XX
CC The present sequence is the human immunoglobulin superfamily protein
CC IGFAM-9 gene, which was isolated from a cDNA library of breast tumour
CC tissue. It is expressed in reproductive, gastrointestinal and immune
CC and haematopoietic tissue, where cancer and inflammation are common. The
CC gene, protein, its antibodies, agonists and antagonists are suitable for
CC diagnosing and treating many diseases, including cancer, immune system
CC disorders (such as inflammation, AIDS, allergies, anaemia,
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC systemic lupus erythematosus and ulcerative colitis), complications of
CC cancer, haemodialysis and extracorporeal circulation, trauma and
CC haematopoietic cancer (such as leukaemia) and infections caused by
CC bacteria, viruses, fungi or parasites.
XX
SQ Sequence 817 BP; 202 A; 237 C; 197 G; 181 T; 0 other;

```

```

Query Match 81.8%; Score 316.6; DB 21; Length 817;
Best Local Similarity 88.6%; Pred. No. 4.4e-87;
Matches 343; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

```

```

QY 1 ATGGACATGAGGCTCCCGCTCAGCTCTGCGGCTCTCTGCTTGCGTCCAGGTGCC 60
DB 11 atggacatgagagctccctcgtcagctccctggtggtctcgtctgtcccaagtgcc 70
QY 61 AGATGTGACATCCAGATGAGCCAGTCTCCATCTCTCCCTGTGTCATGTGAGGAGACAA 120
DB 71 agatgtgacatccagatgagccagctccatctcctcgtctgtcagctctgttggagacaga 130
QY 121 GTTCACCATCTTGACAGGCGCAAGTCAAGACATTAGTATTATTAAATGGTATCAGCAG 180
DB 131 gtccaccatcactgtcggcgagcagcagacattagacattatattagccgtgttcagcag 190
QY 181 AAMCAGGAAAGAGCTCTAGCTCTGATCTATGCTATGCTATCAGTTTGCAAGTGGGGTC 240
DB 191 aaaccagagcagcccttaagctccctgattcattatgacacagcttgcaagtggtgctc 250
QY 241 CCATCAGGTTGACGCGCAGTGTGATCTGGACAGTCTCAGCTCTCAGCAGCCTG 300
DB 251 ccatacaagttcagcgcgctggtgattctggacagattcactctccatcaacagcctg 310
QY 301 CAGCCTGAAGATTCTTGCAGCTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCTTC 360
DB 311 cagcctgaagatttgcacttattactgccaacagcattcattatcctccttacttc 370
QY 361 GGCACAGGAGCCAGCTGGAATCAAA 387
DB 371 ggcgagagagcacaagltgagatcaaa 397

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```

RESULT 15
AA049943
ID AA049943 standard; cDNA; 1066 BP.
XX
AC AA049943;
XX
DT 29-APR-1994 (first entry)
XX
DE Human anti-HBs light chain.
XX
KW Antibody; Ab; light; heavy; chain; hepatitis B;
KW HB; surface antigen; ss.
XX
OS Homo sapiens.
XX
FH Key 33..743 Location/Qualifiers
FT CDS /tag= a
FT sig_peptide /tag= b
FT mat_peptide /tag= c
FT /99..740
FT /note= "claim 1, page 26"
XX
PN WO9320205-A.
XX
PD 14-OCT-1993.
XX
PF 30-MAR-1993; 93WO-JP00396.
XX
PR 30-MAR-1992; 92JP-0074678.
XX
PA (SUNR) SUNTORI LTD.
XX
PI Arima K, Kurihara T, Mtsukura S, Nishihara T, Tsuruoka N;
XX
DR WPI: 1993-336913/42.
DR P-PSDB: AAR42065.
XX
PT Human anti-hepatitis B surface antigen antibody gene - can be
PT used to produce L and H chains of the antibody in large quantity
XX
PS Disclosure; Fig 4-5; 46pp; Japanese.
XX

```

CC Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in AA049943-049944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
XX  
SQ Sequence 1066 BP; 338 A; 274 C; 240 G; 214 T; 0 other;

```
Query Match      81.8%; Score 316.6; DB 14; Length 1066;
Best Local Similarity 88.6%; Pred. No. 4..9e-87;
Matches 343; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1 ATGACATGAGGGTCCCGGCTCAGCTCTGGGCTCCTTCTGCTCTGCTCCAGTGCC 60
   |||||||
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   |||||||

QY 61 AGATGTGACATCCAGATGACCCAGTTCATCTCCCTGCTGATCTGTAGGGACAGA 120
   |||||||
Db 93 aggtgtagacatccagatgacccagctccatctgccaatgctgcatctgtagagacaga 152
   |||||||

QY 121 GTCAACCATCTTGACAGGCAAGTCAGACATTAGTATTATTAAATTGGTATCAGCAG 180
   |||||||
Db 153 gtcaaccatcttgctcgagcgagtcagagcatatattagctggttcagcag 212
   |||||||

QY 181 AAACGAGAAAGCTCCTAGCTCCTGATCTATGTTGATCCAGTTGCAAGTGGGTC 240
   |||||||
Db 213 aaaccgagaaagctccctaagcgctgatactatgctacccagttcgcaagtggggtc 272
   |||||||

QY 241 CCATCAAGGTTTCAGCGGAGTGTGATCTGGACAGAGTTCACTCTCAGCGTACGCGCTG 300
   |||||||
Db 273 ccatacgaggttcagcgagcagtgatctggaacagaatctcaactcacaatcagcagactg 332
   |||||||

QY 301 CAGCCTGAAGATTTTGGCACTTATTACTGCTACAGGTTTATAGTACCCTCGGACGTTT 360
   |||||||
Db 333 cagcctgaagatttggcaacttattactgtacatacataataatcaccgctaagtttc 392
   |||||||

QY 361 GGCCAAGGACCAAGTGGAATCAAA 387
   |||
Db 393 ggcgagggaccaaagtcgagatcaaa 419
   |||
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Job time: 7014 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:47:18 ; Search time 6364.12 Seconds

(without alignments)  
1315.611 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387  
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Sequence: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Scoring table: 21979536 segs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pending Patents, NA, Main: \*

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4	342.2	88.4	729	18	US-09-408-646-135
5	342.2	88.4	729	18	US-09-499-662-125
6	339	87.6	1106	1	PCT-US01-18569-121
7	335.2	86.6	812	30	US-09-760-479-405
8	331.8	85.7	500	32	US-09-834-366-44
9	331.8	85.7	500	58	US-09-197-873-44
10	329.4	85.1	974	32	US-09-859-053-29
11	327.8	84.7	974	30	US-09-760-479-192
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13	327	84.5	391	35	US-09-939-397-2087
14	326.2	84.3	549	26	US-09-665-486-816
15	326.2	84.3	549	55	US-09-472-087-62
16	326.2	84.3	714	18	US-09-168-599-218
17	324.6	83.9	387	1	PCT-US99-09131-27
18	324.6	83.9	387	17	US-09-300-970A-27
19	324.6	83.9	387	34	US-09-905-243-27
20	323	83.4	728	32	US-09-844-684-15
21	322.8	83.4	408	17	US-09-362-510-22815
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23	322.8	83.4	408	34	US-09-904-013-22815
24	321.8	83.2	474	32	US-09-834-366-31
25	321.8	83.2	474	58	US-09-197-873-31
26	321.6	83.1	402	19	US-09-528-409-22604
27	321.6	83.1	402	35	US-09-933-524-22604
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29	321.4	83.0	390	1	PCT-US99-09131-57
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31	321.4	83.0	390	34	US-09-905-243-57

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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33 321.4 83.0 514 37 US-10-066-543-2025 Sequence 2025, Ap  
34 321.4 83.0 537 1 PCT-US02-02870-186 Sequence 186, App  
35 321.4 83.0 537 37 US-10-066-543-186 Sequence 186, App  
36 321.4 83.0 716 32 US-09-844-684-13 Sequence 13, Appl  
37 320.8 82.9 397 19 US-09-528-409-22603 Sequence 22603, A  
38 320.8 82.9 397 35 US-09-933-524-22603 Sequence 22603, A  
39 320.8 82.9 397 35 US-09-933-524-22603 Sequence 22603, A  
40 318.2 82.2 388 11 US-08-728-463-206 Sequence 206, App  
41 318.2 82.2 388 11 US-08-728-463-206 Sequence 206, App  
42 318.2 82.2 388 29 US-09-724-965-206 Sequence 206, App  
43 318.2 82.2 415 16 US-09-274-861-8123 Sequence 8123, Ap  
44 318.2 82.2 415 34 US-09-915-738-8123 Sequence 8123, Ap  
45 318 82.2 936 50 US-60-113-635-20 Sequence 20, Appl

## ALIGNMENTS

RESULT 1  
US-09-019-441-3  
Sequence 3, Application US/09019441  
GENERAL INFORMATION:  
APPLICANT: REF, MITCHELL E.  
KLOETZER, William S.  
NAKAMURA, Takehiko  
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/019,441  
FILING DATE: 05-Feb-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/803,085  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-502  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 387 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..387  
NAME/KEY: mat\_peptide  
LOCATION: 67..387  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-019-441-3

Query Match 100.0%; Score 387; DB 14; Length 387;

Best Local Similarity 100.0%; Pred. No. 7.5e-109;  
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGACATGAGGGTCCCGCTCAGCTCCGCGGCTCCTTCTGCTGGCTCCAGGTGC 60  
1 ATGACATGAGGGTCCCGCTCAGCTCCGCGGCTCCTTCTGCTGGCTCCAGGTGC 60  
Db 1 ATGACATGAGGGTCCCGCTCAGCTCCGCGGCTCCTTCTGCTGGCTCCAGGTGC 60  
QY 61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCGTGTCATCTGTAGGGAGACA 120  
61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCGTGTCATCTGTAGGGAGACA 120  
Db 61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCGTGTCATCTGTAGGGAGACA 120  
QY 121 GTCACCATCATCTTGAGGGGCAAGTACAGACATTTATTTAAATTGGTATAGCAG 180  
121 GTCACCATCATCTTGAGGGGCAAGTACAGACATTTATTTAAATTGGTATAGCAG 180  
Db 121 GTCACCATCATCTTGAGGGGCAAGTACAGACATTTATTTAAATTGGTATAGCAG 180  
QY 181 AACCCAGAAAAAGCTCTAGCTCTGATCTATGTCATCCAGTTCCAAAGTGGGCTC 240  
181 AACCCAGAAAAAGCTCTAGCTCTGATCTATGTCATCCAGTTCCAAAGTGGGCTC 240  
Db 181 AACCCAGAAAAAGCTCTAGCTCTGATCTATGTCATCCAGTTCCAAAGTGGGCTC 240  
QY 241 CCATCAGGTTTCAGCGGCGATGATCTGGACAGAGTTCACTCCAGCAGCCTG 300  
241 CCATCAGGTTTCAGCGGCGATGATCTGGACAGAGTTCACTCCAGCAGCCTG 300  
Db 241 CCATCAGGTTTCAGCGGCGATGATCTGGACAGAGTTCACTCCAGCAGCCTG 300  
QY 301 CAGCTGAAGATTGTGGCACTTATCTGCTACAGGTTTAAATGACCCCTGGACGTT 360  
301 CAGCTGAAGATTGTGGCACTTATCTGCTACAGGTTTAAATGACCCCTGGACGTT 360  
Db 301 CAGCTGAAGATTGTGGCACTTATCTGCTACAGGTTTAAATGACCCCTGGACGTT 360  
QY 361 GCCCAAGGACCAAGGTGAATCAAA 387  
361 GCCCAAGGACCAAGGTGAATCAAA 387  
Db 361 GCCCAAGGACCAAGGTGAATCAAA 387

RESULT 2  
US-09-292-053-5  
Sequence 5, Application US/09292053  
GENERAL INFORMATION:  
APPLICANT: REF, MITCHELL E.  
KLOETZER, WILLIAM S.  
NAKAMURA, TAKEHIKO  
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
FILE REFERENCE: 23522.0699  
CURRENT APPLICATION NUMBER: US/09/292,053  
CURRENT FILING DATE: 1999-04-14  
PRIOR APPLICATION NUMBER: 08/803,085  
PRIOR FILING DATE: 1997-02-20  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 5  
LENGTH: 387  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: (1)..(67)  
NAME/KEY: mat\_peptide  
LOCATION: (67)..(387)  
NAME/KEY: CDS  
LOCATION: (1)..(387)  
US-09-292-053-5

Query Match 100.0%; Score 387; DB 16; Length 387;  
Best Local Similarity 100.0%; Pred. No. 7.5e-109;  
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGACATGAGGGTCCCGCTCAGCTCCGCGGCTCCTTCTGCTGGCTCCAGGTGC 60  
1 ATGACATGAGGGTCCCGCTCAGCTCCGCGGCTCCTTCTGCTGGCTCCAGGTGC 60  
Db 1 ATGACATGAGGGTCCCGCTCAGCTCCGCGGCTCCTTCTGCTGGCTCCAGGTGC 60  
QY 61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCGTGTCATCTGTAGGGAGACA 120  
61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCGTGTCATCTGTAGGGAGACA 120  
Db 61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCGTGTCATCTGTAGGGAGACA 120

Oy	121	GTACACCACTCTTCAGAGGGCAAGCAGAGCACTTAGTGTATTATTTAAATTGGTATCAGAC	180
Db	121	gtcaccaatcactcttcagagggcaagtcagagacatctagttataatctaattgaatcgaag	180
Oy	181	AAACCAAGGAAAAAGTCCTTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAGTGGGGTC	240
Db	181	aaacccaagaaaaagctcccttaagctctcatgtatcttgatccacagtttgcaaatgtagtgc	240
Oy	241	CCATCAAGCTTCAGGGGAGTGATGCGGACAGATGTTCACTCTCACCCTGACAGAGCTG	300
Db	241	ccatcaagagttcagcgcgcagctgagatctcggagcagaagttcaatccacacgctcagaagctcg	300
Oy	301	CAGCCTGAAGATTTTTGCGACTTATTACTGTCFACAGGTTTATATAGTACCCCTCGACGCTTC	360
Db	301	cagcctgaagatcttcgacactattactgctctacaggtttatagttaccctctgagcgttc	360
Oy	361	GGCCAAAGGACCAAGTGGAATCAAA	387
Db	361	ggccaaaggacccaagctggaatcaaaa	387

### RESULT 3

```

: Sequence 3, Application US/09343485A
:
: GENERAL INFORMATION:
:
: APPLICANT: REEF, MITCHELL R.
: APPLICANT: BARNETT, RICHARD S.
: APPLICANT: MCILCHIAN, KAREN R.
:
: TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
:
: TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
:
: TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
:
: FILE REFERENCE: 037003-0275807
:
: CURRENT APPLICATION NUMBER: US/09/343,485A
:
: CURRENT FILING DATE: 1999-06-30
:
: PRIOR APPLICATION NUMBER: 09/023,715
:
: PRIOR FILING DATE: 1998-02-13
:
: PRIOR APPLICATION NUMBER: 08/819,866
:
: PRIOR FILING DATE: 1997-03-14
:
: NUMBER OF SEQ ID NOS: 3
:
: SOFTWARE: PatentIn Ver. 2.1
:
: SEQ ID NO: 3
:
: LENGTH: 19040
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
:
: OTHER INFORMATION: referred to as "Wandy"
:
: US-09-343-485A-3

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Query Match	100.0%	Score 387	DB 17	Length 19040
Best Local Similarity	100.0%	Pred. No. 3.2e-108		
Matches 387	Conservative	0	Mismatches 0	Indels 0
Gaps				
QY	1	ATGACATGAGGGGCCCGCTCAGCTCCTTGAGGGCTCTTCGTGCTGGCTGCCAGGTGCC	60	
Db	7545	atgagcatgaggggccccgcgtcagctctcttctggtctctcttctgtcttgcgtcccaagtgcc	760	
QY	61	AGATGTGACATCCAGATGACCAAGTCTTCATCTTCCCTGTCTGCATCTGTAGGGGACAG	120	
Db	7605	agatgtgacatccagatgacccagctccatcttccctgtctgcatctgtlaagggacaga	766	
QY	121	GTCACATCACTTTCAGGGGCAAGTCAGACATTAGATATTAAATTGATTCAGCAG	180	
Db	7665	gtcacatcacttgcaggggcaagtcagagacattlaagatlaattlaattgtatcagcag	772	
QY	181	AAACGAGGAAAAAGCTCTTAAGCTTCATCTATATTGTCATCATAGTTGCAAAATGGGGTTC	240	
Db	7725	aaacggagaaaagctcttaagcttcctatgtctatgttgcacagcttgcgaagtgggtc	778	
QY	241	CCATCAAGGTTCACGGCAGTGGATCTGGGACAGATTCACTCTACACGTCACAGACTTG	300	

Db 7785 ccacaaaggttcaagcggcagttgactcgtggacagagttcaactcaccgtcaegacgctg 7844  
QY 301 CAGCTTGAAGATTTTGGACTTATTTACTGTCCTCAGAGTTTATAGTACCCCTGGAGCTTC 360  
Db 7845 cagcttgaagattttggaacttaactactgctcaggttatacgtaccctcgtgacgttc 7904  
QY 361 GGCCTAAGGACCAAGTGTGMAATCAAA 367  
Db 7905 ggccaaagagaccaggtcgaatactcaaa 7931

## RESULT 4

```

1  GENERAL: 125, Application US/09408646A
2  -----
3  APPLICANT: Serizawa, Nobufusa
4  APPLICANT: Horiyama, Hiroyuki
5  APPLICANT: Nakahara, Kaori
6  APPLICANT: Tamaki, Ikuko
7  APPLICANT: Takahashi, Toru
8  TITLE OF INVENTION: Anti-Fas Antibodies
9  FILE REFERENCE: 990540/HG
10 CURRENT APPLICATION NUMBER: US/09/408,646CR
11 CURRENT FILING DATE: 1999-09-30
12 EARLIER APPLICATION NUMBER: JP 10-276881
13 EARLIER FILING DATE: 1998-09-30
14 NUMBER OF SEQ ID NOS: 165
15 SEQ ID NO 125
16 -----
17 LENGTH: 729
18 -----
19 TYPE: DNA
20 ORGANISM: Homo sapiens
21 US-09-408-646-125

```

Query match	88.4%;	Score 342.2;	DB 18;	Length 729;
-------------	--------	--------------	--------	-------------

OY	1	ATNASACATGAGAGGATCCCGGCTACACTCTCGGGGCTCTCTTCGCTCTGGGCTCCAGGATGCC	60
Db	7	atggacacagaaaggtcccccgcctgcgtccctggggcttcctgcgaactctggctccagaggtcc	66
OY	61	AGATGTGACATCCAGATGATACCAGTCTCTCATTCTCCCTGTCTGCATCTGTAGAGGAGACA	120
Db	67	agatgtgacatccagatgataccagcttccatccctcctgtctgcatctgtatagagaagaaga	126
OY	121	GTACACCATCTACTGCAAGGGCAAGTCAGACACTTAGTATTATTTAAATTGGTATCAGCAG	180
Db	127	gtcacccactctgcgcggcgaagtcagacatagcagctatttaattggtatcagcag	186
OY	181	AAACCGAGAAAGATCCCTAACCTCTGATATCATGTGCATCCATCCATTTGCAAAAGTGGGTC	240
Db	187	aaacccaggaagaaagccctaaagcttccttgatctatgctgcatacagcttgcgaagtgagggc	246
OY	241	CCATCAAGGTTTCAGCGGACATGATGTGGAGCAGAGTTTCATCTCACCCTCAGCAGCCTG	300
Db	247	ccatcaaggttcagttgtagagtgatctcgggacaaattcaactccacatcagagctgtg	306
OY	301	CAGCCTGAAGATTTTTCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCGTTC	360
Db	307	caacctgaaagattctgcgaactactactgctcaacacagagttacagttacccctcgaagcttc	366
OY	361	GGCCAAAGGACCAAGGTGGAAATCAA	387
Db	367	ggccaaaggaaccaaggtggaatcaaa	393

## RESULT 5

```
US-09-499-662-125
; Sequence 125, Application US/094996625
; GENERAL INFORMATION:
; APPLICANT: Serizawa, Nobufusa
; APPLICANT: Haruyama, Hideyuki
```

```

: APPLICANT: Nakahara, Kacori
: APPLICANT: Tamaki, Ikuro
: APPLICANT: Takahashi, Tohru
: TITLE OF INVENTION: Anti-Pas Antibodies
: FILE REFERENCE: 980126C1P/HG
: CURRENT APPLICATION NUMBER: US/09/499,662
: CURRENT FILING DATE: 2000-02-09
: EARLIER APPLICATION NUMBER: US 09/053,583
: EARLIER FILING DATE: 1998-04-01
: NUMBER OF SEQ ID NOS: 165
: SEQ ID NO 125
: LENGTH: 729
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-499-662-125

```

Query Match	88.4%	Score 342.2	DB 18	Length 729
Best Local Similarity	97.8%	Pred No. 7.2e-95		
Matches 359	Conservative	0	Mismatches 28	Indels 0
			Gaps	0

QY	1	ATGACATAGAGGGTCCCGCGCTCAGCTCTGGGGGCTCTTTCGCTGGTCCAGGTGCC	60
Db	7	atgacatagaggggtcccgcgctcagctctctgggggctcttctgcgtgggtccaggtgcc	66
QY	61	AGATGTGATCCAGATGATGCCAATCTTCATCTTCCCTGTCTGCATCTGTAGGGACAGA	120
Db	67	agatgtgatccagatgatgccaatcttccatcttccctctctgtcatctgtagagacaga	126
QY	121	GTCACCATCTTTCGAGGGCAAGTCAGACATTTAGATTTATTTAAATTGGTATCACAG	180
Db	127	gtcacccatcttgcgaggcaagtcagagacattcagcatattgaattgatacagcag	186
QY	181	AAACAGGAAAGATCTCTTAAGCTCTCATCTATGTCATTCATCCAGATTGGCAAGGGGTC	240
Db	187	aaacaggaaagatctcttaagctctcatctatgctcatccagtttcgcaagtggggtc	246
QY	241	CCATCAAGGTTCAAGCGGAGTGTGATCTGGGACAGAGTTCACTCAACCGTCAGCAGCGCTG	300
Db	247	ccatcaaggttcagttgcagtgagttctcggacagattccactccaccatcaagagtcig	306
QY	301	CAGCTGAAGATTTTGGACTTATTACTGTCTACAGCTTTATAGTACCCCTCGAGCGTTC	360
Db	307	caacctgaagattttgcaccttactactgtloaacagagttacagttacccctcgaagcttc	366
QY	361	GGCCAGGAGGACCAAGGTGGAAATCAA	387
Db	367	ggccaggagggaccgaagtcggaatcaaa	393

```

RESULT      6
PCT-US01-18569-121
Sequence 121, Application PC/US0118569
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: P4133PCT
CURRENT APPLICATION NUMBER: PCT/US01/18569
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 121
LENGTH: 1106
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (302)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (424)

```

```

: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (1039)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (1084)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: SITE
: LOCATION: (1103)
: OTHER INFORMATION: n equals a,t,g, or c
PCT-US01-18569-121

```

Query Match	87.6%;	Score 339;	DB 1;	Length 1106;
Best Local Similarity	90.7%;	Pred. No. 8.2e-94;		
Matches 351;	Conservative	7;	Mismatches 29;	Indels 0;
			Gaps	0

QY	1	ATGACATGAGGGGCCCCGGCTACACCTCTGGGGGCTCTTGGCTCTGGGCTCCAGAGGCC	60
Db	79	atggacatgagggccccggctacacctctgggggctcttggctctgggctccagaggcc	138
QY	61	AGATGATACATCCAGATGACCCCATCTCCATCTCCCTGTCTGCATCTGTAGGGGACAGA	120
Db	139	agatgtagatccagatgagaccagttccatccctctgtcatctgttagagacaga	198
QY	121	GTCACCATCTACCTGCAGGCGCAGTCAGGACATTAGTATTATTTAAATTGGTATCAGAG	180
Db	199	gtcaccatctacttcgcgggaacgacagagatttgcaacatttaattgtaacagcag	258
QY	181	AAACACGAGAAAGCTCCTTAAGCTCCGTATGATTTGTCATTCGAGTTGCAAGAGGGGGTC	240
Db	259	aaacacgagaaagcctcctaagctcttcgtatctcaagtcacatccatttgcagaagtgggttc	318
QY	241	CCATCAAGGTTCAACGGCAGTGTGATCTGGGACAGAGTTCTACTCTCACGCTCAGACGCTG	300
Db	319	ccatcaaggttcagttgctgcagtgatgctcgggacagatttcaactcagcagcgtc	378
QY	301	CAGCCTCAAGATTTTGGGACTTATTACTGTCTACAGGTTTAAATAGTACCCCTCGAGCTTC	360
Db	379	carcctgaagatttgcgaacttactgactgcacaacagatgataatnccctctcaacttc	438
QY	361	GGCCAGGAGCAAGGTGGGAATAAA	387
Db	439	ggccaggagaccaaggtcgagatcaaa	465

```

RESULT 7
US-09-760-479-405
Sequence 405, Application US/09760479
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT253
CURRENT FILING DATE: 2001-01-16
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 946
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 405
LENGTH: 812
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (201)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (792)
OTHER INFORMATION: n equals a,t,g, or c
US-09-760-479-405

```

Query Match	86.68;	Score 335.2;	DB 30;	Length 812;
-------------	--------	--------------	--------	-------------

Best Local Similarity 90.2%; Pred. No. 1,1e-92;  
Matches 349; Conservative 7; Mismatches 31; Indels 0; Gaps 0;

OY 1 ATGGACATGAGGCTCCCGCTCAGCTCTGGGGCTCTCTGCTGGCTCCAGGTGCC 60  
DB 41 atggacatgaggtcccgctcagctctggggctctctgctggctccaggtgcc 100  
OY 61 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCGATCTGTAGGGACAGA 120  
DB 101 agatgtgacatccagatgacccagctctccctgtcgtcgtatctgtagagacaga 160  
OY 121 GTCACCATCTTGGACGGCAAGTACGACATTAGTATTATTTAAATTGGTACGAC 180  
DB 161 gtccacatcacttgcgggcaagtcagacatgacacatlttaattgtagatcagcag 220  
OY 181 AAACCGAAGAAAGCTCTAGCTAGCTGATCTATGTTGATCCAGTTGCAAGTGGGGTC 240  
DB 221 aaacccgaaagcccttaccctcagctcctgctgacacatltgcaaaatggggctc 280  
OY 241 CCATCAAGGTTGACGGCGAGTGGATCTGGAGACAGCTTCTCAGCGTCAAGCCTG 300  
DB 281 ccatacaggttcagtcagtcagtcgctggagacagatltcacttcaaccatcagtcg 340  
OY 301 CAGCCTGAAGATTTCGCGACTTATTCTGCTACAGGTTTATAGTACCCCTGGAGCTTC 360  
DB 341 caacctgaagatttgcgaacttactactgtcaacagaaatlwastlaaccctcgacgttc 400  
OY 361 GGCCAGGAGGACCAAGGTGAATCAAA 387  
DB 401 ggccaaaggagcaaggtggaatcaaa 427

RESULT 8  
US-09-834-366-44  
; Sequence 44, Application US/09834366  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/834,366  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/197,873  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 44  
; LENGTH: 500  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 28..498  
; NAME/KEY: sig\_peptide  
; LOCATION: 28..93  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 13.600003814697  
; OTHER INFORMATION: seq LGILLMLNGARC/DI  
US-09-834-366-44

Query Match 85.7%; Score 331.8; DB 32; Length 500;  
Best Local Similarity 86.0%; Pred. No. 1e-91;  
Matches 333; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

OY 1 ATGGACATGAGGCTCCCGCTCAGCTCTGGGGCTCTCTGCTGGCTCCAGGTGCC 60  
DB 28 atggacatgaggtcccgctcagctctggggctctctgctggctccaggtgcc 87  
OY 61 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCGATCTGTAGGGACAGA 120

DB 88 agatgtgacatccagatgacccagctcctcctcctgctgacatcgtggagacaga 147  
OY 121 GTCACCATCTTGGACGGCAAGTACGACATTAGTATTATTTAAATTGGTACGAC 180  
DB 148 gtccacatcacttgcgggcaagtcagacatltakrcrgctwttaamtgtatcagctc 207  
OY 181 AAACCGAAGAAAGCTCTAGCTGATCTATGTTGATCCAGTTGCAAGTGGGGTC 240  
DB 208 aaacccgaaagcccttaccctcagctcctgctgacacatlttgaagaatgggctc 267  
OY 241 CCATCAAGGTTGACGGCGAGTGGATCTGGAGACAGATTCTCAGCGTCAAGCCTG 300  
DB 268 ccatacaggttcagtcagtcagtcgctggagacagatltcacttcaaccatcagcagtcg 327  
OY 301 CAGCCTGAAGATTTCGCGACTTATTCTGCTACAGGTTTATAGTACCCCTGGAGCTTC 360  
DB 328 caacctgaagatttgcgaacttactactgtcaacagaaatlwastlaaccctcgacgttc 387  
OY 361 GGCCAGGAGGACCAAGGTGAATCAAA 387  
DB 388 ggccmaggagcaagktggarltcarr 414

RESULT 9  
US-60-197-873-44  
; Sequence 44, Application US/60197873  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.US1.PRO  
; CURRENT APPLICATION NUMBER: US/60/197,873  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 44  
; LENGTH: 500  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 28..498  
; NAME/KEY: sig\_peptide  
; LOCATION: 28..93  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 13.600003814697  
; OTHER INFORMATION: seq LGILLMLNGARC/DI  
US-60-197-873-44

Query Match 85.7%; Score 331.8; DB 58; Length 500;  
Best Local Similarity 86.0%; Pred. No. 1e-91;  
Matches 333; Conservative 26; Mismatches 28; Indels 0; Gaps 0;

OY 1 ATGGACATGAGGCTCCCGCTCAGCTCTGGGGCTCTCTGCTGGCTCCAGGTGCC 60  
DB 28 atggacatgaggtcccgctcagctctggggctctctgctggctccaggtgcc 87  
OY 61 AGATGTGACATCCAGATGACCCAGTCTCCCTGTCGATCTGTAGGGACAGA 120  
DB 88 agatgtgacatccagatgacccagctctccctgtcgtatctgtagagacaga 147  
OY 121 GTCACCATCTTGGACGGCAAGTACGACATTAGTATTATTTAAATTGGTACGAC 180  
DB 148 gtccacatcacttgcgggcaagtcagacatltakrcrgctwttaamtgtatcagctc 207  
OY 181 AAACCGAAGAAAGCTCTAGCTGATCTATGTTGATCCAGTTGCAAGTGGGGTC 240  
DB 208 aaacccgaaagcccttaccctcagctcctgctgacacatlttgaagaatgggctc 267



SEQ ID NO 2087  
LENGTH: 391  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-289-768-2087

Query Match 84.5%; Score 327; DB 16; Length 391;  
Best Local Similarity 90.9%; Pred. No. 2.9e-90;  
Matches 348; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGCTCCCGCTAGCTCTCTGCGCTCTTCTGCTCTGCTCCAGGTC 60  
DB 9 atggacatgagggctcccgctcagctcctcgggctcctcgtactctggtccgaggtgc 68  
QY 61 AGATGTGACATTCAGATGAGCCAGTCTCCATCTCCCTGCTCAGTCTAGGAGGACAGA 120  
DB 69 agatgtgacatccagatgagccagctccatcctcctcgtcagctcgtagaagacaga 128  
QY 121 GTTCACATCATCTGACAGGCGCAAGTCAAGCATTAGTATTATTAAATTGATACAGAG 180  
DB 129 gtacacatcctctgcgggcaagtcagagcattagcagcatttaattgtagcagcag 188  
QY 181 AACCCAGGAAAGCTCTAGCTCTGATCTGATGTCATGTCATGTCATGTCATGTCATGTC 240  
DB 189 aaaccaggaaagccctcctcagctcctcagctcagctcagctcagctcagctcagctc 248  
QY 241 CCATCAAGGTTTACGCGCACTGATCTGGAGACAGATTCATCTCAACCTGACAGCTG 300  
DB 249 ccatacaagttcagtgagctgagctcgtgagacagattcactcctcaccacagcagctg 308  
QY 301 CACCTGAGAGATTTTGGACTTATTACTGCTCTACAGGTTTATAGTACCCCTCGAGCTTC 360  
DB 309 caacctgaaagatttgcacacttactcgtcacaagagttacagctcccgctacactt 368  
QY 361 GGCCAAAGGACCAAGTGGAAT 383  
DB 369 ggcacaggagaccaaagctgagat 391

RESULT 13  
US-09-939-397-2087  
Sequence 2087, Application US/09939397  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
FILE REFERENCE: 20411-765  
CURRENT APPLICATION NUMBER: US/09/939,397  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: 09/289,768  
PRIOR FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 39996  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2087  
LENGTH: 391  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-939-397-2087

Query Match 84.5%; Score 327; DB 35; Length 391;  
Best Local Similarity 90.9%; Pred. No. 2.9e-90;  
Matches 348; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGACATGAGGCTCCCGCTAGCTCTCTGCGCTCTTCTGCTCTGCTCCAGGTC 60  
DB 9 atggacatgagggctcccgctcagctcctcgggctcctcgtactcctcagctcagaggtgc 68  
QY 61 AGATGTGACATTCAGATGAGCCAGTCTCCATCTCCCTGCTCAGTCTAGGAGGACAGA 120  
DB 69 agatgtgacatccagatgagccagctccatcctcctcgtcagctcgtagaagacaga 128

QY 121 GTTCACATCATCTGACAGGCGCAAGTCAAGCATTAGTATTATTAAATTGATACAGAG 180  
DB 129 gtacacatcctctgcgggcaagtcagagcattagcagcatttaattgtagcagcag 188  
QY 181 AACCCAGGAAAGCTCTAGCTCTGATCTGATGTCATGTCATGTCATGTCATGTCATGTC 240  
DB 189 aaaccaggaaagccctcctcagctcctcagctcagctcagctcagctcagctcagctc 248  
QY 241 CCATCAAGGTTTACGCGCACTGATCTGGAGACAGATTCATCTCAACCTGACAGCTG 300  
DB 249 ccatacaagttcagtgagctgagctcgtgagacagattcactcctcaccacagcagctg 308  
QY 301 CACCTGAGAGATTTTGGACTTATTACTGCTCTACAGGTTTATAGTACCCCTCGAGCTTC 360  
DB 309 caacctgaaagatttgcacacttactcgtcacaagagttacagctcccgctacactt 368  
QY 361 GGCCAAAGGACCAAGTGGAAT 383  
DB 369 ggcacaggagaccaaagctgagat 391

RESULT 14  
US-09-665-486-816  
Sequence 816, Application US/09665486  
GENERAL INFORMATION:  
APPLICANT: Hodgson, David M.  
APPLICANT: Lincoln, Stephen E.  
APPLICANT: Russo, Frank D.  
APPLICANT: Spiro, Peter A.  
APPLICANT: Banville, Steve C.  
APPLICANT: Bracher, Shawn R.  
APPLICANT: Dufour, Gerard E.  
APPLICANT: Cohen, Howard J.  
APPLICANT: Rosen, Bruce H.  
APPLICANT: Shah, Purvi  
APPLICANT: Chalup, Michael S.  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Jones, Anissa L.  
APPLICANT: Yu, Jimmy Y.  
APPLICANT: Greenawalt, Lila B.  
APPLICANT: Panzer, Scott R.  
APPLICANT: Roseberry, Ann M.  
APPLICANT: Wright, Rachel J.  
APPLICANT: Chen, Wensheng  
APPLICANT: Liu, Tommy F.  
APPLICANT: Yap, Pierre E.  
APPLICANT: Stockdreher, Theresa K.  
APPLICANT: Amshy, Stefan  
APPLICANT: Fong, Willy T.  
TITLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES  
FILE REFERENCE: PT-0076 US  
CURRENT APPLICATION NUMBER: US/09/665,486  
CURRENT FILING DATE: 2000-09-20  
PRIOR APPLICATION NUMBER: 60/156,297  
PRIOR FILING DATE: 1999-09-24  
PRIOR APPLICATION NUMBER: 60/156,624  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: 60/156,625  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: 60/168,599  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: 60/168,197  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: 60/168,614  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: 60/168,611  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: 60/168,613  
PRIOR FILING DATE: 1999-12-02  
NUMBER OF SEQ ID NOS: 958  
SOFTWARE: PERL Program  
SEQ ID NO 816  
LENGTH: 549





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:58:47 : Search time 662.78 Seconds

(without alignments)  
1881.788 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387  
Sequence: 1 ATGGACATGAGGTCCTCCG.....GGACCAAGTGAATCAAA 387

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents, NA, New: \*  
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2: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq: \*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq: \*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	387	100.0	729	US-10-103-686-3	Sequence 3, Appl
2	342.2	88.4	729	US-10-216-484-125	Sequence 125, Appl
3	335.2	86.6	812	US-10-206-008-405	Sequence 405, App
4	327.8	84.7	974	US-10-206-008-192	Sequence 192, App
5	326.2	84.3	714	US-10-153-382-18	Sequence 18, Appl
6	323	83.5	728	US-10-040-244-15	Sequence 15, Appl
7	321.4	83.0	514	US-10-214-403-2025	Sequence 2025, Ap
8	321.4	83.0	537	US-10-214-403-186	Sequence 186, App
9	321.4	83.0	716	US-10-040-244-13	Sequence 29, Appl
10	318	82.2	936	US-09-831-805A-29	Sequence 29, Appl
11	316.6	81.8	917	US-09-831-805A-28	Sequence 28, Appl
12	316.4	81.8	917	US-09-831-805A-20	Sequence 20, Appl
13	311.8	80.6	698	US-10-040-244-11	Sequence 11, Appl
14	311.8	80.6	944	US-09-602-148A-48	Sequence 48, Appl
15	310	80.1	634	US-10-158-646-55	Sequence 55, Appl
16	309.8	79.8	520	US-10-146-502-1210	Sequence 1210, Ap
17	308.8	79.8	378	US-10-175-525-55	Sequence 55, Appl
18	308.4	78.6	705	US-09-335-697B-16	Sequence 16, Appl
19	304.2	78.4	928	US-09-831-805A-32	Sequence 32, Appl
20	303.6	78.0	494	US-10-146-502-1811	Sequence 1811, Ap
21	302	77.6	918	US-10-206-008-111	Sequence 111, App
22	300.4	77.3	490	US-09-918-995-37859	Sequence 37859, A
23	299	77.3	819	US-10-158-646-65	Sequence 65, Appl
24	298.8	77.2	583	US-10-198-846-8365	Sequence 8365, Ap
25	298.8	77.2	583	US-10-198-846-8365	Sequence 8365, Ap

26	295	76.2	576	7	US-10-175-525-65	Sequence 65, Appl
27	295	76.2	3123	7	US-10-175-525-101	Sequence 101, App
28	289.2	74.7	372	7	US-10-175-525-78	Sequence 78, Appl
29	287.8	74.4	916	5	US-09-831-805A-24	Sequence 24, Appl
30	287.4	74.3	463	7	US-10-146-502-2039	Sequence 2039, Ap
31	286.2	74.0	890	5	US-09-831-805A-31	Sequence 31, Appl
32	285	73.6	384	7	US-10-089-500-30	Sequence 30, Appl
33	284.8	73.6	454	1	PCT-US02-18947-1918	Sequence 1918, Ap
34	284.4	73.6	454	7	US-10-172-118-1918	Sequence 1918, Ap
35	283.4	73.2	384	7	US-10-089-500-39	Sequence 39, Appl
36	281.8	72.8	384	7	US-10-089-500-27	Sequence 27, Appl
37	281.8	72.8	384	7	US-10-089-500-33	Sequence 33, Appl
38	281.8	72.8	384	7	US-10-089-500-42	Sequence 42, Appl
39	280.4	72.5	853	7	US-10-158-646-68	Sequence 68, Appl
40	279.4	72.2	720	5	US-09-511-939-1	Sequence 1, Appl
41	279.4	72.2	720	5	US-09-968-561A-1	Sequence 1, Appl
42	279.2	72.1	369	5	US-09-918-995-7569	Sequence 7569, Ap
43	279	72.1	438	6	US-10-198-846-5398	Sequence 5398, A
44	278.8	72.0	614	5	US-09-919-002-12346	Sequence 12346, A
45	278.6	72.0	384	7	US-10-089-500-36	Sequence 36, Appl

## ALIGNMENTS

RESULT 1  
US-10-103-686-3  
Sequence 3, Application US/10103686  
GENERAL INFORMATION:  
APPLICANT: REFE, Mitchell E.  
KLOETZER, William S.  
TAKAMURA, Takehiko  
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/103,686  
FILING DATE: 25-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/803,085  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 387 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..387  
FEATURE:  
NAME/KEY: mat\_peptide

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RESULT      3
US-10-206-008-405
; Sequence 405, Application US/10206008
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT2531N
; CURRENT APPLICATION NUMBER: US/10/206,008
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
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; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
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; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924

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2 PRIOR APPLICATION NUMBER: 60/224,518  
3 PRIOR FILING DATE: 2000-08-14  
4 PRIOR APPLICATION NUMBER: 60/236,369  
5 PRIOR FILING DATE: 2000-09-29  
6 PRIOR APPLICATION NUMBER: 60/224,519  
7 PRIOR FILING DATE: 2000-08-14  
8 PRIOR APPLICATION NUMBER: 60/220,964  
9 PRIOR FILING DATE: 2000-07-26  
10 PRIOR APPLICATION NUMBER: 60/241,809  
11 PRIOR FILING DATE: 2000-10-20  
12 PRIOR APPLICATION NUMBER: 60/249,299  
13 PRIOR FILING DATE: 2000-11-17  
14 PRIOR APPLICATION NUMBER: 60/236,327  
15 PRIOR FILING DATE: 2000-09-29  
16 PRIOR APPLICATION NUMBER: 60/241,785  
17 PRIOR FILING DATE: 2000-10-20  
18 PRIOR APPLICATION NUMBER: 60/244,617  
19 PRIOR FILING DATE: 2000-11-01  
20 PRIOR APPLICATION NUMBER: 60/225,268  
21 PRIOR FILING DATE: 2000-08-14  
22 PRIOR APPLICATION NUMBER: 60/236,368  
23 PRIOR FILING DATE: 2000-09-29  
24 PRIOR APPLICATION NUMBER: 60/251,856  
25 PRIOR FILING DATE: 2000-12-08  
26 PRIOR APPLICATION NUMBER: 60/251,868  
27 PRIOR FILING DATE: 2000-12-08  
28 PRIOR APPLICATION NUMBER: 60/229,344  
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30 PRIOR APPLICATION NUMBER: 60/234,997  
31 PRIOR FILING DATE: 2000-09-25  
32 PRIOR APPLICATION NUMBER: 60/229,343  
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34 PRIOR APPLICATION NUMBER: 60/229,345  
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36 PRIOR APPLICATION NUMBER: 60/229,287  
37 PRIOR FILING DATE: 2000-09-01  
38 PRIOR APPLICATION NUMBER: 60/229,513  
39 PRIOR FILING DATE: 2000-09-05  
40 PRIOR APPLICATION NUMBER: 60/231,413  
41 PRIOR FILING DATE: 2000-09-08  
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50 PRIOR APPLICATION NUMBER: 60/236,370  
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52 PRIOR APPLICATION NUMBER: 60/236,802  
53 PRIOR FILING DATE: 2000-10-02  
54 PRIOR APPLICATION NUMBER: 60/237,037  
55 PRIOR FILING DATE: 2000-10-02  
56 PRIOR APPLICATION NUMBER: 60/237,040  
57 PRIOR FILING DATE: 2000-10-02  
58 PRIOR APPLICATION NUMBER: 60/240,960  
59 PRIOR FILING DATE: 2000-10-20  
60 PRIOR APPLICATION NUMBER: 60/239,935  
61 PRIOR FILING DATE: 2000-10-13  
62 PRIOR APPLICATION NUMBER: 60/239,937  
63 PRIOR FILING DATE: 2000-10-13  
64 PRIOR APPLICATION NUMBER: 60/241,787  
65 PRIOR FILING DATE: 2000-10-20  
66 PRIOR APPLICATION NUMBER: 60/246,474  
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68 PRIOR APPLICATION NUMBER: 60/246,532  
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70 PRIOR APPLICATION NUMBER: 60/249,216  
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72 PRIOR APPLICATION NUMBER: 60/249,210  
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1 PRIOR APPLICATION NUMBER: 60/226,681  
2 PRIOR FILING DATE: 2000-08-22  
3 PRIOR APPLICATION NUMBER: 60/225,759  
4 PRIOR FILING DATE: 2000-08-14  
5 PRIOR APPLICATION NUMBER: 60/225,213  
6 PRIOR FILING DATE: 2000-08-14  
7 PRIOR APPLICATION NUMBER: 60/227,182  
8 PRIOR FILING DATE: 2000-08-22  
9 PRIOR APPLICATION NUMBER: 60/225,214  
10 PRIOR FILING DATE: 2000-08-14  
11 PRIOR APPLICATION NUMBER: 60/235,836  
12 PRIOR FILING DATE: 2000-09-27  
13 PRIOR APPLICATION NUMBER: 60/230,438  
14 PRIOR FILING DATE: 2000-09-06  
15 PRIOR APPLICATION NUMBER: 60/215,135  
16 PRIOR FILING DATE: 2000-06-30  
17 PRIOR APPLICATION NUMBER: 60/225,266  
18 PRIOR FILING DATE: 2000-08-14  
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61 PRIOR APPLICATION NUMBER: 60/232,401  
62 PRIOR FILING DATE: 2000-09-14  
63 PRIOR APPLICATION NUMBER: 60/241,808  
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65 PRIOR APPLICATION NUMBER: 60/241,826  
66 PRIOR FILING DATE: 2000-10-20  
67 PRIOR APPLICATION NUMBER: 60/241,786  
68 PRIOR FILING DATE: 2000-10-20  
69 PRIOR APPLICATION NUMBER: 60/241,221

;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,475  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/231,243  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,065  
  
Query Match 86.6%; Score 335.2; DB 6; Length 812;  
Best Local Similarity 90.2%; Pred. No. 2,2e-91;  
Matches 349; Conservative 7; Mismatches 31; Indels 0; Gaps 0;  
  
QY 1 ATGACATGAGGGTCCCGCTCAGCTCTCTGGGCTCCTTGTGCTCTGGCTCCAGGGTCC 60  
Db 41 atgacatgaggggtcccgctcagctctctgggctccttgtgctctggctccaggggtcc 100  
QY 61 AGATGTACATTCAGATGACCCAGCTTCATCTTCCTGCTGCTGATGAGGAGAGA 120  
Db 101 agatgtacattcagatgacccagcttcattcttcctgctgctgactctgctcagagtc 160  
QY 121 GTACACATCTTCAGAGGCAAGTACAGACATTAGTATTATTTAAATGGTATCAGCAG 180  
Db 161 gtacacatcttccagagggcaagtacagacattagttatattttaaattgtatcagcag 220  
QY 181 AATCCAGAAAGCTCTTAAGCTCTATGTATGTTCATTCAGATTGGCAAGTGGGCTC 240  
Db 221 aatccagaaagctcttaagctctatgtatgtttcatcttcagatttgcacaaagtgggtc 280  
QY 241 CCATCAAGGTTTCAGCGGAGTGTGATGTGGAGAGTTCACCTCTCAGCGCAGCAGCTG 300  
Db 281 ccataaggttcagcgagtgatgtggtgagacagattctcactccacacatcattgtctg 340  
QY 301 CAGCCTAAGATTTTGGAGCTTATTACTGTCTACAGTGTATAGTACCCTCGAGCTTC 360  
Db 341 cagcctaagattttggagcttattactgtctacaggttattagttaccctcgagcttc 400  
QY 361 GGCCAAGGAGCAAGTGTGAATCAA 387  
Db 401 ggccaaggagcaagtgtgaatacaaa 427  
  
RESULT 4  
US-10-206-008-192  
; Sequence 192, Application US/10206008  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT253C1N  
; CURRENT APPLICATION NUMBER: US/10/206,008  
; CURRENT FILING DATE: 2002-07-29  
; PRIOR APPLICATION NUMBER: 09/760,479  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22

;; PRIOR APPLICATION NUMBER: 60/216,647  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,267  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/216,880  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,270  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/251,869  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/235,834  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: 60/234,274  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: 60/234,223  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: 60/228,924  
;; PRIOR FILING DATE: 2000-08-30  
;; PRIOR APPLICATION NUMBER: 60/224,518  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/236,369  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/224,519  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/220,964  
;; PRIOR FILING DATE: 2000-07-26  
;; PRIOR APPLICATION NUMBER: 60/241,809  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/249,299  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/236,327  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/241,785  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/244,617  
;; PRIOR FILING DATE: 2000-11-01  
;; PRIOR APPLICATION NUMBER: 60/225,268  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/236,368  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/251,856  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/251,868  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/229,344  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/234,997  
;; PRIOR FILING DATE: 2000-09-25  
;; PRIOR APPLICATION NUMBER: 60/229,343  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,345  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,287  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,513  
;; PRIOR FILING DATE: 2000-09-05  
;; PRIOR APPLICATION NUMBER: 60/231,413  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/229,509  
;; PRIOR FILING DATE: 2000-09-05  
;; PRIOR APPLICATION NUMBER: 60/236,367  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/237,039  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,038  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/236,370  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/236,802  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,037  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,040



ORGANISM: Homo sapiens  
US-10-153-382-18

Query Match 84.3%; Score 326.2; DB 7; Length 714;  
Best Local Similarity 90.2%; Pred. No. 1.2e-88;  
Matches 34; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGACATGAGGCTCCCGCTACGCTCTGCGGCTCTTCTGCTGCTGCCAGAGTGC 60  
Db 1 atgacatgaggtcccgctcagctccttgggctctcgtactcttgcgcgaggtgc 60  
QY 61 AGATGTGACATCCAGATACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGAGACA 120  
Db 61 agatgtacatccagatccagatccatcccttgccttgccttgccttgccttgccttgc 120  
QY 121 GTCAACATCACTTGCAGGCAAGTACAGACATTAAGTATTAATTTAGTATCAGCAG 180  
Db 121 gtcaacatcacttgcagggcaagtcagacatlaacagctattagatgtatcagcag 180  
QY 121 gtcaacatcacttgcagggcaagtcagacatlaacagctattagatgtatcagcag 180  
Db 121 gtcaacatcacttgcagggcaagtcagacatlaacagctattagatgtatcagcag 180  
QY 181 AACCCAGAAAAGCTCCTTAAGCTCTGATCTATGTTCATCCAGTTTGCAAGTGGGCTC 240  
Db 181 aaaccaggaagccccaactcctgctatgctgcatccagtttgcaagtgaggctc 240  
QY 241 CCATCAGGCTTCAGCGCAGTGGATCTGGGACAGATTCATCTCACCCTGACAGCCTG 300  
Db 241 ccatacaggttcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 300  
QY 301 CAGCCTGACAGATTTTGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCCTG 360  
Db 301 caactgtgaagtttgcactactactgtcaacagatattcagtaactcactcacttc 360  
QY 361 GGCCAAGGACCAAGTGGAAATCAA 387  
Db 361 ggccttgagcaagaagtggaatcaaa 387

## RESULT 6

US-10-040-244-15  
Sequence 15, Application US/10040244  
GENERAL INFORMATION:  
APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
APPLICANT: FORCE, WALKER P.  
APPLICANT: TAKAHASHI, NOBUAKI  
APPLICANT: MIKAYAMA, TOSHIFUMI  
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBODI  
FILE REFERENCE: 021286/0272501  
CURRENT APPLICATION NUMBER: US/10/040,244  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: 60/200,601  
PRIOR FILING DATE: 2000-4-28  
PRIOR APPLICATION NUMBER: PCT/US01/13672  
PRIOR FILING DATE: 2001-04-27  
PRIOR APPLICATION NUMBER: 09/844,684  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 3.0  
SEQ ID NO 15  
LENGTH: 728  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-040-244-15

Query Match 83.5%; Score 323; DB 7; Length 728;  
Best Local Similarity 89.7%; Pred. No. 1.1e-87;  
Matches 34; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 ATGACATGAGGCTCCCGCTACGCTCTGCGGCTCTTCTGCTGCTGCCAGAGTGC 60  
Db 59 atgacatgaggtcccgctcagctccttgggctctcgtactcttgcgcgaggtgc 60  
QY 61 AGATGTGACATCCAGATACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGAGACA 120

Db 119 agatgtacatccagatccagatccatcccttgccttgccttgccttgccttgccttgc 178  
QY 121 GTCAACATCACTTGCAGGCAAGTACAGACATTAAGTATTAATTTAGTATCAGCAG 180  
Db 121 gtcaacatcacttgcagggcaagtcagacatlaacagctattagatgtatcagcag 180  
QY 181 AACCCAGAAAAGCTCCTTAAGCTCTGATCTATGTTCATCCAGTTTGCAAGTGGGCTC 240  
Db 181 aaaccaggaagccccaactcctgctatgctgcatccagtttgcaagtgaggctc 240  
QY 241 CCATCAGGCTTCAGCGCAGTGGATCTGGGACAGATTCATCTCACCCTGACAGCCTG 300  
Db 241 ccatacaggttcagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcgagtcg 300  
QY 301 CAGCCTGACAGATTTTGGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGAGCCTG 360  
Db 301 caactgtgaagtttgcactactactgtcaacagatattcagtaactcactcacttc 360  
QY 361 GGCCAAGGACCAAGTGGAAATCAA 387  
Db 419 ggccttgagcaagaagtggaatcaaa 445

## RESULT 7

US-10-214-403-2025  
Sequence 2025, Application US/10214403  
GENERAL INFORMATION:  
APPLICANT: Jiang, Yuguo  
APPLICANT: Chenault, Ruth A.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Indrias, Carol Yoseph  
APPLICANT: Lodes, Michael J.  
APPLICANT: Secrist, Heather  
APPLICANT: Carter, Darick  
APPLICANT: Fanger, Gary R.  
APPLICANT: Smith, Carole L.  
APPLICANT: Durham, Margalita  
APPLICANT: Stolk, John A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER  
FILE REFERENCE: 210121.563CI  
CURRENT APPLICATION NUMBER: US/10/214,403  
CURRENT FILING DATE: 2002-08-06  
NUMBER OF SEQ ID NOS: 3420  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2025  
LENGTH: 514  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-214-403-2025

Query Match 83.0%; Score 321.4; DB 6; Length 514;  
Best Local Similarity 89.4%; Pred. No. 3e-87;  
Matches 34; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1 ATGACATGAGGCTCCCGCTACGCTCTGCGGCTCTTCTGCTGCTGCCAGAGTGC 60  
Db 12 atgacatgaggtcccgctcagctccttgggctctcgtactcttgcgcgaggtgc 60  
QY 61 AGATGTGACATCCAGATACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGAGACA 120  
Db 72 agatgtacatccagatccagatccatcccttgccttgccttgccttgccttgccttgc 120  
QY 121 GTCAACATCACTTGCAGGCAAGTACAGACATTAAGTATTAATTTAGTATCAGCAG 180  
Db 121 gtcaacatcacttgcagggcaagtcagacatlaacagctattagatgtatcagcag 180  
QY 132 gtcaacatcacttgcagggcaagtcagacatlaacagctattagatgtatcagcag 191  
Db 181 AACCCAGAAAAGCTCCTTAAGCTCTGATCTATGTTCATCCAGTTTGCAAGTGGGCTC 240  
Db 192 aaaccaggaagccccaactcctgctatgctgcatccagtttgcaagtgaggctc 251



Query Match	82.2%	Score 318	DB 5:	Length 936
Best Local Similarity	90.3%	Pred. No.	3.8e-86	
Matches	352	Conservative	35	Indels 3
		Mismatches	0	Gaps 1

RESULT 11  
US-09-831-805A-28  
; Sequence 28, Application US/09831805A  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE PHARMACEUTICALS, INC

APPLICANT: TANG, Y. Tom  
APPLICANT: CORLETT, Neil C.  
APPLICANT: GUEGLER, Karl J.  
APPLICANT: GORGONE, Gina A.  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: LU, Dyung Alina M.  
APPLICANT: LAL, Preeti  
APPLICANT: HILLMAN, Jennifer L.

Query Match	81.8%	Score 316.6	DB 5	Length 817
Best Local Similarity	88.6%	Pred. No. 9.7e-86		
Matches 343	Conservative 0	Mismatches 44	Indels 0	Gaps 0

OY	1	ATGACATGAGGGGCCCCGGCTCAGGCTCTCAGGGGCTCCTTCCTCGGCTCCAGAGTGC	60
Db	11	atgacatgagggatcctcctgcctcaagctcccgaggctctcctcgtctctgtttcccaagtgcc	70
OY	61	AGATGTGACATCCAGATGATGACCCAGTCTCCATCTTCCCTGTGCACTGTGAGGGACAGA	120
Db	71	agatgtgacatccagatgagaccagcttcacatcctcactgtctgcatactgttgagacaga	130
OY	121	GTCACCATCTGACCTTGACAGGGCAAGTCAGAGCAATTAGTATTATTAAATTTGGATCAGAG	180
Db	131	gtcacccatcacttgctcgaggagctcagacatgacaattatctagctcgtgtttcaagag	190
OY	181	AAACACGAGAAAGTGCTCTAGCTCCCGATCTATGTGGTCACAGTTGGCAAGTGGGGTC	240
Db	191	aaacacgaggaagcgcctctaagctcccgactatgatacacaagttgcgaagtgaggctc	250
OY	241	CCATCAAGGTTTCAGCGGCACTGATCTGGGACAGATTCATCTCAGCGTCAGCAGCTTG	300
Db	251	ccatcaagttcagcgcgcagtgatactgtggaagatcttcacctccatcacatcaacgcctg	310
OY	301	CAGCTCAAGATTTTGGGACTTATTACTGCTACAGGTTTATAGTACCCCTCGACGCTTC	360
Db	311	cagcctcaagaattctcaacttactcacaacagcatcatagtatcctccttacttc	370
OY	361	GGCCAGAGGACCAAGGTGGAATCAAA	387
Db	371	ggcggaggagccaagtcgagatcca	397

RESULT 12  
US-09-831-805A-20  
Sequence 20 Application US/09931805A  
GENERAL INFORMATION:  
APPLICANT: INCYTE PHARMACEUTICALS, INC.  
APPLICANT: YUE, Henry  
APPLICANT: TANG, Y.-Tom  
APPLICANT: CORLEY, Neil C.  
APPLICANT: GUEGLER, Karl J.  
APPLICANT: GORGONE, Gina A.  
APPLICANT: BAUGHN, Mariah R.  
APPLICANT: LU, Dyung Anna M.  
APPLICANT: IAL, Preeti  
APPLICANT: HILLMAN, Jennifer L.  
APPLICANT: YANG, Junming  
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS  
FILE REFERENCE: PF-0643 PCP  
CURRENT APPLICATION NUMBER: US/09/831, 805A  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBERS: 09/195,853; unassigned; 60/113,635; 60/128,194  
PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07



NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PERL Program  
SEQ ID NO 20  
LENGTH: 917  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID NO: 079785CBI  
US-09-831-805A-20

Query Match 81.8%; Score 316.4; DB 5; Length 917;  
Best Local Similarity 90.0%; Pred. No. 1.2e-85;  
Matches 351; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

1 ATGACATGAGGAGTCCCGCTCAGCTCCTGAGGCTCTTCTGCTGGCTCCGAGTGCC 60  
14 atgacatgaggggtcccgctcagctcctctgggctcctctgactctggtccgaagtgcc 73  
61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCCTGTGCATCTGTAGGGACAGA 120  
74 agatgtgacatccagatgaccagctccatccctctgctgcatctgtagagacaga 133  
121 GTACCATCACTTGACAGGCGAAGTCAAGATTAAGTATTAAATTGATATCAGCAG 180  
134 gtacatcacacttgcgagaggtcagagcatctagcagcatctaaattgtagcagcag 193  
181 AAACGAGGAAGAGCTCTAGACTCTGATCTATGTTGATGATTCAGATTGCAAGTGGGCTC 240  
194 aaacgaggaagagcccttaagctccctgactatctatgctgacatccagattgcaagtggggtc 253  
241 CCATCAAGTTTACGCGGACGTGATCTGGACAGAGTTTCACTCTACCGTCAGCAGCTG 300  
254 ccataagtttaccggtcagtgagctgagcagattcactcaccatcagcagctg 313  
301 CAGCCTGAAGATTTGGACTTATCTACTCTACAGTTTATAGTACCCTCGG--ACG 357  
314 cagcctgaagatttggacttacttactctactgtcaacagagctacccctcgcagcacc 373  
358 TTCGGCCAAAGGACCAAGTGTGAATCAAA 387  
374 ttccggccaaggagacagcagctggaatcaa 403

RESULT 13  
US-10-040-244-11  
Sequence 11, Application US/10040244  
GENERAL INFORMATION:  
APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
APPLICANT: FORCE, WALKER F.  
APPLICANT: TAKAHASHI, NOBUAKI  
APPLICANT: MIKAWAMA, TOSHIYUKI  
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD  
FILE REFERENCE: 021286/0272501  
CURRENT APPLICATION NUMBER: US/10/040, 244  
CURRENT FILING DATE: 2002-06-17  
PRIOR APPLICATION NUMBER: 60/200, 601  
PRIOR FILING DATE: 2000-4-28  
PRIOR APPLICATION NUMBER: PCT/US01/13672  
PRIOR FILING DATE: 2001-04-27  
PRIOR APPLICATION NUMBER: 09/844, 684  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 3.0  
SEQ ID NO 11  
LENGTH: 698  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-040-244-11

Query Match 80.6%; Score 311.8; DB 7; Length 698;

Best Local Similarity 87.9%; Pred. No. 2.6e-84;  
Matches 340; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

1 ATGACATGAGGAGTCCCGCTCAGCTCCTGAGGCTCTTCTGCTGGCTCCGAGTGCC 60  
29 atgacatgaggggtcccgctcagctcctctgggctcctctgctgctcgtcccgagtgcc 88  
61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCCTGTGCATCTGTAGGGACAGA 120  
89 aatgtgacatccagatgaccagctccctccaccctctgctgcatctgtagagacaga 148  
121 GTACCATCACTTGACAGGCGAAGTCAAGATTAAGTATTAAATTGATATCAGCAG 180  
149 gtacatcacacttgcgagagccagtcagatctgagtaacctgttgccgtgtagcagcag 208  
181 AAACGAGGAAGAGCTCTAGACTCTGATCTATGTTGATGATTCAGATTGCAAGTGGGCTC 240  
209 aaacgaggaagagcccttaagctccctgctctataaagcactctgtttagaagtggtc 268  
241 CCATCAAGTTTACGCGGACGTGATCTGGACAGAGTTTCACTCTACCGTCAGCAGCTG 300  
269 ccataagtttaccggtcagtgagctgagcagaaatcactcaccatcacaacagcctg 328  
301 CAGCCTGAAGATTTGGACTTATCTACTCTACAGTTTATAGTACCCTCGAGCTTC 360  
329 cagcctgaagatttggacttacttactgtcacaacagctcattatctcgtgagcgtc 388  
361 GGCCAAAGGACCAAGTGTGAATCAAA 387  
389 ggcacaaggagcaaggtggaatcaaa 415

RESULT 14  
US-09-602-148A-48  
Sequence 48, Application US/09602148A  
GENERAL INFORMATION:  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Jiang, Yugu  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.482  
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER  
CURRENT APPLICATION NUMBER: US/09/602, 148A  
CURRENT FILING DATE: 2002-04-09  
NUMBER OF SEQ ID NOS: 126  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 48  
LENGTH: 944  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-602-148A-48

Query Match 80.6%; Score 311.8; DB 5; Length 944;  
Best Local Similarity 87.9%; Pred. No. 2.9e-84;  
Matches 340; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

1 ATGACATGAGGAGTCCCGCTCAGCTCCTGAGGCTCTTCTGCTGGCTCCGAGTGCC 60  
13 atgacatgaggggtcccgctcagctcctctgggctcctctgactctggtccgaagtgcc 72  
61 AGATGTGACATCCAGATGACCCAGTCTCATCTTCCCTGTGCATCTGTAGGGACAGA 120  
73 agatgtgacatccagatgaccagctccatccctctgctgcatctgtagagacaga 132  
121 GTACCATCACTTGACAGGCGAAGTCAAGATTAAGTATTAAATTGATATCAGCAG 180  
133 gtacatcacacttgcgagagccagtcagatctgagtaacctcttaattgtagcagcaa 192  
181 AAACGAGGAAGAGCTCTAGACTCTGATCTATGTTGATGATTCAGATTGCAAGTGGGCTC 240  
193 aaacgaggaagagccctcagctccctgactatctatcactcattatctgcaagtgggtc 252  
241 CCATCAAGTTTACGCGGACGTGATCTGGACAGAGTTTCACTCTACCGTCAGCAGCTG 300

Search completed: September 23, 2002, 19:58:52  
Job time: 7182 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 18:00:51 ; Search time 110.65 Seconds  
(without alignments)  
859,107 Million cell updates/sec

Title: US-09-019-441-3

Perfect score: 387

Sequence: 1 ATGGACATGAGGTCCCGC.....GGACCAAGTGAATCAAA 387

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/lna/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/lna/5A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/lna/5B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/lna/PCUTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	387	100.0	387	3	US-08-803-085-3
2	318.2	82.2	388	4	US-09-042-353-358
3	318.2	82.2	388	4	US-08-758-417A-206
4	316.6	81.8	1066	1	US-08-157-101A-4
5	308.6	79.7	387	1	US-08-217-918-1
6	307	79.3	439	4	US-09-042-353-360
7	307	79.3	439	4	US-08-758-417A-208
8	304.2	78.6	705	1	US-08-488-376-16
9	304.2	78.6	705	2	US-08-634-223-16
10	304.2	78.6	705	2	US-08-634-224-16
11	304.2	78.6	705	2	US-08-634-400-16
12	304.2	78.6	705	2	US-08-635-878-16
13	304.2	78.6	705	2	US-08-770-057-16
14	304.2	78.6	705	4	US-09-335-697B-16
15	302	78.0	420	4	US-09-042-353-420
16	302	78.0	420	4	US-08-758-417A-220
17	302	78.0	3819	4	US-09-042-353-393
18	302	78.0	3819	4	US-08-758-417A-243
19	297.4	76.8	390	2	US-08-646-367-2
20	296.2	76.5	384	1	US-08-259-372A-13
21	296.2	76.5	384	1	US-08-468-671-13
22	279.4	72.2	324	2	US-08-378-939-23
23	278.2	71.9	708	1	US-08-488-376-18
24	278.2	71.9	708	2	US-08-634-223-18
25	278.2	71.9	708	2	US-08-634-224-18
26	278.2	71.9	708	2	US-08-634-400-18
27	278.2	71.9	708	2	US-08-635-878-18

28	278.2	71.9	708	2	US-08-770-057-18	Sequence 18, Appl
29	278.2	71.9	708	4	US-09-335-697B-18	Sequence 18, Appl
30	273.8	70.7	381	2	US-08-621-751A-5	Sequence 5, Appl
31	269.6	69.7	321	4	US-09-240-274-102	Sequence 102, Appl
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33	269.6	69.7	321	4	US-09-240-274-221	Sequence 221, Appl
34	269.6	69.7	321	4	US-09-240-274-222	Sequence 222, Appl
35	269	69.5	382	3	US-08-836-561-70	Sequence 70, Appl
36	268.6	69.4	401	1	US-08-472-788A-47	Sequence 47, Appl
37	268.6	69.4	401	1	US-08-472-788A-47	Sequence 47, Appl
38	268.6	69.4	401	1	US-08-477-531B-47	Sequence 47, Appl
39	268.6	69.4	401	2	US-08-082-842A-47	Sequence 47, Appl
40	268	69.3	321	4	US-09-240-274-105	Sequence 105, Appl
41	266.4	68.8	321	4	US-09-240-274-107	Sequence 107, Appl
42	266.4	68.8	321	4	US-09-240-274-216	Sequence 216, Appl
43	265	68.5	324	2	US-08-378-939-17	Sequence 17, Appl
44	264.8	68.4	321	4	US-09-240-274-98	Sequence 98, Appl
45	264.8	68.4	321	4	US-09-240-274-104	Sequence 104, Appl

#### ALIGNMENTS

RESULT 1  
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; Sequence 3, Application US/08803085  
; Patent No. 6011138  
; GENERAL INFORMATION:  
; APPLICANT: REFF, Mitchell E.  
; APPLICANT: KLOETZER, William S.  
; APPLICANT: NAKAMURA, Takehiko  
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/803,085  
; FILING DATE: 20-FEB-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; TELEPHONE: (703) 836-6620  
; TELECOMMUNICATION INFORMATION:  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 387 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..387  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 67..387  
; US-08-803-085-3

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Query Match Similarity      100.0%; Score 387; DB 3; Length 387;
Best Local Similarity      100.0%; Pred. No. 8.4e-113; Indels      0;
Matches 387; Conservative  0; Mismatches 0; Indels      0; Gaps      0

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QY      61 AATGTGACATCCAGATGATACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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DB       121 GTACCATCTACTTGCAGGGCAAGTCAGGACATAGGTATTTAAATGGTATCGACG 180
QY      181 AAACGAGGAAAAAGCTCTTAAGCTCTGATCTATGTTGCATCCAGTTTGGCAAGTGGGGTC 240
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DB       181 AAACGAGGAAAAAGCTCTTAAGCTCTGATCTATGTTGCATCCAGTTTGGCAAGTGGGGTC 240
QY      241 CCATCAAGGTTAGGGGCGAGTGGATCTGGGACAGAGTTACTCTACCGCTCAGCAGCGTCG 300
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QY      301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCTCGGAGGTC 360
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QY      361 GGGCAAGGAGGACCAAGGTGGAAATCAA 387
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DB       361 GGGCAAGGAGGACCAAGGTGGAAATCAA 387

RESULT      2
US-09-042-353-358
; Sequence 358, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042.353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131

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Query Match	Best Local Similarity	Matches 344: Conservative	Score 82.2%	DB 4: Indels	Length 388:	Gaps 0:
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Db 301 CAGCCTGAGATTGTTGGACTTATTACTGTCTACAGGCTTATAGTATCCCGTACACTTT 360  
QY 361 GGGCAAGGACCAAGGTGGAATCAAA 387  
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RESULT 3  
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; Patent No. 6300129  
; GENERAL INFORMATION:  
; APPLICANT: Lonberg, Nils  
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
; Producing Heterologous Antibodies  
; NUMBER OF SEQUENCES: 417  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/758,417A  
; FILING DATE: 02-Dec-1996  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/728,463  
; FILING DATE: 10-OCT-1996  
; APPLICATION NUMBER: US 08/544,404  
; FILING DATE: 10-OCT-1995  
; APPLICATION NUMBER: US 08/352,322  
; FILING DATE: 07-DEC-1994  
; APPLICATION NUMBER: US 08/209,741  
; FILING DATE: 09-MAR-1994  
; APPLICATION NUMBER: US 08/165,699  
; FILING DATE: 10-DEC-1993  
; APPLICATION NUMBER: US 08/161,739  
; FILING DATE: 03-DEC-1993  
; APPLICATION NUMBER: US 08/155,301  
; FILING DATE: 18-NOV-1993  
; APPLICATION NUMBER: US 08/096,762  
; FILING DATE: 22-JUL-1993  
; APPLICATION NUMBER: US 08/053,131  
; FILING DATE: 26-APR-1993  
; APPLICATION NUMBER: US 07/990,860  
; FILING DATE: 16-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Serafini, Andrew T.  
; REGISTRATION NUMBER: 41,303  
; REFERENCE/DOCKET NUMBER: 014643-009030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 206:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 388 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 206:

US-08-758-417A-206  
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Best Local Similarity 88.9%; Pred. No. 4e-91;  
Matches 344; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
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Db 361 GGGCAGGGGACCAAGCTGAGATCAAA 387  
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RESULT 4  
US-08-157-101A-4  
; Sequence 4, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENDI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION  
; TITLE OF INVENTION: PLASMIDS THEREFOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARILAN K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUCH

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? TELEPHONE: (415) 326-2400
? TELEFAX: (415) 326-2422
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 387 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: single
?     TOPOLOGY: linear
?     MOLECULE TYPE: cDNA
?     HYPOTHEICAL: NO
?     ANTI-SENSE: NO
?     FEATURE:
?     NAME/KEY: CDS
?     LOCATION: 1..387
?     US-08-217-918-1
?
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Best Local Similarity 87.3%; Pred. No. 4.2e-88;
Matches 338; Conservative 0; Mismatches 49; Indels 0; Caps 0;
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QY      61  AGATGTGACATCCAGATGATCCAGCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
Db      61  AATGTGACATCCAGATGATACCAGCTCTCCACACCGTGTCTGCATCTGTAGGAGACAGA 120
QY      121  GTACACATCACTTTCGACGGGCAAGTCAGGACACTTAAAGTATTTAAATTGGTATCAGCAG 180
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QY      181  AAACAGGAAAGTCCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGGAAAGGGGGTC 240
Db      181  AACAGCAGGAAAGCCCTTAACATCATGATCTATAAGCGCTATTTAGAAATGGGGTC 240
QY      241  CCATCAAGGTTTCAGCGGCAAGTGATCTGGGACAGAGTTCACTCTACCGTCAGCAGCCTG 300
Db      241  CCATCAAGGTTTCAGCGGCAAGTGATCTGGGACAGAAATTCACCTCCACCATCAGCAGCCTG 300
QY      301  CAGCTGAAGTTTGGGACCTTATTACTGTCTACAGGTTTATTAACCCCGGAGGTTTC 360
Db      301  CAGCTGAAGTTTGGCACTTATTACTGTCTACAGGTTTATTAACAGTATTAAGATTATTCCTGGACGTTTC 360
QY      361  GGCCAGGAGACCAAGGTGGAATCAAA 387
Db      361  GGCCAGGAGACCAAGGTGGAATCAAA 387
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? Sequence 360, Application US/09042353
? Patent No. 6255458
?
GENERAL INFORMATION:
? APPLICANT: Lonberg, M11s
? APPLICANT: Kay, Robert M.
? TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
?     TITLE OF INVENTION: Producing Heterologous Antibodies
? NUMBER OF SEQUENCES: 421
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
?
COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:

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1 APPLICATION NUMBER: US/09/042,353
2 FILING DATE: 13-MAR-1998
3 CLASSIFICATION: 800
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: US 07/810,279
6 FILING DATE: 17-DEC-1991
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 07/853,408
9 FILING DATE: 18-MAR-1992
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 07/904,068
12 FILING DATE: 23-JUN-1992
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/990,860
15 FILING DATE: 16-DEC-1992
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/053,131
18 FILING DATE: 26-APR-1993
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/096,762
21 FILING DATE: 22-JUL-1993
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/155,301
24 FILING DATE: 18-NOV-1993
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/161,739
27 FILING DATE: 03-DEC-1993
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/165,699
30 FILING DATE: 10-DEC-1993
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/209,741
33 FILING DATE: 09-MAR-1994
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 08/352,322
36 FILING DATE: 07-DEC-1994
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 08/544,404
39 FILING DATE: 10-OCT-1995
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 08/728,463
42 FILING DATE: 10-OCT-1996
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: WO PCT/US96/16433
45 FILING DATE: 10-OCT-1996
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: US 08/758,417
48 FILING DATE: 02-DEC-1996
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: WO PCT/US97/21803
51 FILING DATE: 01-DEC-1997
52 ATTORNEY/AGENT INFORMATION:
53 NAME: Apple, Randolph T.
54 REGISTRATION NUMBER: 36,429
55 REFERENCE/DOCKET NUMBER: 014643-009040US
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: (415) 576-0200
58 TELEFAX: (415) 576-0300
59 INFORMATION FOR SEQ ID NO: 360:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 439 base pairs
62 TYPE: nucleic acid
63 STRANDEDNESS: single
64 TOPOLOGY: linear
65 MOLECULE TYPE: DNA
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Query Match	79.38%	Score 307;	DB 4;	Length 439.
Best Local Similarity	87.18%	Pred. No. 1.4e-87;		
Matches 33/;	Conservative	0;	Mismatches 50;	Indels 0;
Gaps				

1 ATGACATGAGGGTCCCCGCTCAGCTCTCGGGGCTCTTTCGCTTCGGCTCCAGGTGCC 60

Db	1	ATGACATGAGAGTCCCGGTTACAGTCCCTGGGGGCTCTGGCTCTCTGTTCCAGAGTGC	60
Qy	61	AGATGTACATCCAGATGACCACCTCTCCATCTTCCCTGTCGTGATCTGTAGGGGACAGA	120
Db	61	AGAGTACATCCAGATGACCACCTCTCCATCTTCCCTGTCGTGATCTGTAGGGGACAGA	120
Qy	121	GTCACATCACTTCAGGGCAAGCAGGACATTAGTATTATTTAAATGGTATACAGCAG	180
Db	121	GTCACATCACTTCGTGGGGAGTCAGGGATATTAGCAGCTGTGAGCTGTATCAGCAG	180
Qy	181	AAACCAAGAAAAGCTCTCTAAGCTCTGATCTATGTTGCATCCAGTTTGCAAAAGTGGGTC	240
Db	181	AAACCAAGAAAAGCCCTTAAGTCCCTATCTATCTCATCCAGTTTGCAAAAGTGGGTC	240
Qy	241	CCATCAAGGTTACAGGGCAGTGGATCTGGGGACAGATTCACACTCAGCAGAGAGCTG	300
Db	241	CCATCAAGGTTACAGGGCAGTGGATCTGGGGACAGATTTCACTCTCAGCAGATCAGAGCTG	300
Qy	301	CAGCGTGAAGATTTTGGGACTTATTACTGTCACAGGTTATAGTACCCTCGGACGTTC	360
Db	301	CAGCGTGAAGATTTTGGCACTTATTACTGCCAACAGATATGATTAACCCGTACACTTTT	360
Qy	361	GGCCAAAGGACCAAGGTGGAATATAA	387
Db	361	GGCCAGGGACCAAGCTGGAGATATAA	387

RESULT 7  
 US-08-758-417A-208  
 Sequence 208, Application US/08758417A  
 Patent No. 6300129  
 GENERAL INFORMATION:  
 APPLICANT: Lomborg, Nils  
 Kay, Robert M.  
 TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
 Producing Heterologous Antibodies  
 NUMBER OF SEQUENCES: 417  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 City: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/758,417A  
 FILING DATE: 02-Dec-1996  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/728,463  
 FILING DATE: 10-OCT-1996  
 APPLICATION NUMBER: US 08/544,404  
 FILING DATE: 10-OCT-1995  
 APPLICATION NUMBER: US 08/352,322  
 FILING DATE: 07-DEC-1994  
 APPLICATION NUMBER: US 08/209,741  
 FILING DATE: 09-MAR-1994  
 APPLICATION NUMBER: US 08/165,699  
 FILING DATE: 10-DEC-1993  
 APPLICATION NUMBER: US 08/161,739  
 FILING DATE: 03-DEC-1993  
 APPLICATION NUMBER: US 08/155,301  
 FILING DATE: 18-NOV-1993  
 APPLICATION NUMBER: US 08/096,762  
 FILING DATE: 22-JUL-1993  
 APPLICATION NUMBER: US 08/053,131  
 FILING DATE: 26-APR-1993

APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 208:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 439 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 208:  
US-08-758-417A-208

Query Match 79.3%; Score 307; DB 4; Length 439;  
Best Local Similarity 87.1%; Pred. No. 1.4e-87;  
Matches 337; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 ATGACATGAGGTCCTCCGCTCAGCTCTGCGGCTCTCTGCTGCTGCTCCAGGTGCC 60  
DB 1 ATGGACATGAGTTCCTCCGCTCAGCTCTGCGGCTCTCTGCTGCTGCTCCAGGTGCC 60  
QY 61 AGATGTGATCCAGATGAGCCAGTCCATCTTCCCTGCTGCTGCTGATGAGGAGACA 120  
DB 61 AGATGTGATCCAGATGAGCCAGTCCATCTTCCCTGCTGCTGCTGATGAGGAGACA 120  
QY 121 GTCCACATCTGTCAGAGGCAAGTACAGACATAGTATTATTAAATGGTATCAGCAG 180  
DB 121 GTCCACATCTGTCAGAGGCAAGTACAGACATAGTATTATTAAATGGTATCAGCAG 180  
QY 181 AAGCCAGGAAAGCTCTAAGCTCCGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 181 AAGCCAGGAAAGCTCTAAGCTCCGATGATGATGATGATGATGATGATGATGATGAT 240  
QY 241 CCATCAGGTTGAGCGGAGTGTGAGGAGAGTTCAGTCTCAGCCGTCAGAGCTG 300  
DB 241 CCATCAGGTTGAGCGGAGTGTGAGGAGAGTTCAGTCTCAGCCGTCAGAGCTG 300  
QY 301 CAGCTGAAAGATTTTCGACTTATTAAGTCTGTAAGGTTAAGTACCCCTCGAGCTTC 360  
DB 301 CAGCTGAAAGATTTTCGACTTATTAAGTCTGTAAGGTTAAGTACCCCTCGAGCTTC 360  
QY 361 GGGCAGGAGGCAAGGTGGAATCAAA 387  
DB 361 GGGCAGGAGGCAAGGTGGAATCAAA 387

RESULT 8

US-08-488-376-16  
Sequence 16, Application US/08488376  
Patent No. 5811524  
GENERAL INFORMATION:  
APPLICANT: BRAMS, Peter  
APPLICANT: CHAMAT, Souleima Salim  
APPLICANT: PAN, Li-Zhen  
APPLICANT: WALSH, Edward E.  
APPLICANT: HEARD, Cheryl Janne  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND  
METHODS OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia

COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,376  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-150  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 705 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..705  
US-08-488-376-16

Query Match 78.6%; Score 304.2; DB 1; Length 705;  
Best Local Similarity 87.4%; Pred. No. 1.3e-86;  
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCGCTCAGCTCTGCGGCTCTCTGCTGCTGCTCCAGGTGCCAGATG 66  
DB 1 ATGGAGACCTCTGCTCAGCTCTGCGGCTCTCTGCTGCTGCTCCAGGTGCCAGATG 60  
QY 67 GACATCCAGATGAGCCAGTCTCCATCTTCCCTGCTGCTGCTGATGAGGAGCAGAGTCAC 126  
DB 61 GACATCCAGATGAGCCAGTCTCCATCTTCCCTGCTGCTGCTGATGAGGAGCAGAGTCAC 120  
QY 127 ATCATTGAGGCGCAAGTACAGCATTAGTATTATTAAATGGTATCAGCAGAAACCA 186  
DB 121 ATCATTGAGGCGCGAGTACAGCATTAGTATTATTAAATGGTATCAGCAGAAACCA 180  
QY 187 GGAAGGCTCTAAGCTCCGATGATGATGATGATGATGATGATGATGATGATGAT 246  
DB 181 GGAAGGCTCTAAGCTCCGATGATGATGATGATGATGATGATGATGATGATGAT 240  
QY 247 AGGTGAGCGGAGTGTGAGGAGAGTTCAGTCTCAGCCGTCAGAGCTGAGCCT 306  
DB 241 AGGTGAGCGGAGTGTGAGGAGAGTTCAGTCTCAGCCGTCAGAGCTGAGCCT 300  
QY 307 GAAGATTTTTCGACTTATTAAGTCTGTAAGGTTAAGTACCCCTCGAGCTTCGGCCAA 366  
DB 301 GAAGATTTTTCGACTTATTAAGTCTGTAAGGTTAAGTACCCCTCGAGCTTCGGCCAA 360  
QY 367 GGGACCAAGGTGGAATCAAA 387  
DB 361 GGGACCAAGGTGGAATCAAA 381

RESULT 9

US-08-634-223-16  
Sequence 16, Application US/08634223  
Patent No. 5840298  
GENERAL INFORMATION:  
APPLICANT: BRAMS, Peter  
APPLICANT: CHAMAT, Souleima Salim  
APPLICANT: PAN, Li-Zhen  
APPLICANT: WALSH, Edward E.





Db 121 ATCACTGGCCGGCAGCTGACAGAGATTGCTAGTTAATTGATATGATCAGCAACAACCA 180  
QY 187 GGAAGAGCTCTTAAGCTCTGATCTATGTGATCCAGTTGGCAAGTGGGGTCCCATCA 246  
Db 181 GGGAAAGCCCCCTAAGCTCTGATATATGCTGATCCCAATTTGACACCGTGGGGTCCCATCA 240  
QY 247 AGGTACAGCGAGTGGATCTGGGACAGAGTTCACTCTCACCGCTGACAGCCCTGACAGCT 306  
Db 241 AGGTTCAGTGGCGGTGATCTGGGACAGATTTCATCTCCATCAACAGTCTGCAACCT 300  
QY 307 GAAGATTTTCCACTATATCTCTACAGGTTATAGTACCCCTGGAGCTGGGCCCA 366  
Db 301 GAAGATTTTCCACTATATCTCTACAGGTTATAGTACCCCTGGAGCTGGGCCCA 360  
QY 367 GGGACCAAGGTGGAAATCAAA 387  
Db 361 GGGACCAAGGTGGAAATCAAA 381

## RESULT 11

US-08-634-400-16

Sequence 16, Application US/08634400

Patent No. 5939068

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter  
APPLICANT: CHAMAT, Soulaïma Salim  
APPLICANT: PAN, Li-Zhen  
APPLICANT: WALSH, Edward E.  
APPLICANT: HEARD, Cheryl Janne  
APPLICANT: NEWMAN, Roland Anthony  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND  
NUMBER OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P. O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22113-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,400  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/488,376  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-150  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ. ID NO.: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 705 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..705  
US-08-634-400-16

Query Match 78.6%; Score 304.2; DB 2; Length 705;  
Best Local Similarity 87.4%; Pred. No. 1.3e-86;  
Matches 333; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 7 ATGAGGTCCTCCCTAAGCTCTGAGGCTCTCTCTCTGCTGCTCCAGTGCAGATGT 66  
Db 1 ATGAGACCCCTCTAGCTCTGAGGCTCTCTCTCTCTCTCTGCTGCTCCAGTGCAGATGT 60  
QY 67 GACATCCAGATGACCCAGTCTCCATCTTCCCTCTGATCTGATAGGAGAGATGACCC 126  
Db 61 GACATCCAGATGACCCAGTCTCCATCTTCCCTCTGATCTGATAGGAGAGATGACCC 120  
QY 127 ATCACTGGACAGGCAAGTACAGCAATTAGTATTAATTGATATGATCAGAGAAACCA 186  
Db 121 ATCACTGGACAGGCAAGTACAGCAATTAGTATTAATTGATATGATCAGAGAAACCA 180  
QY 187 GGAAGAGCTCTTAAGCTCTGATCTATGTGATCCAGTTTGAAGTGGGGTCCCATCA 246  
Db 181 GGGAAAGCCCCCTAAGCTCTGATATATGCTGATCCCAATTTGACACCGTGGGGTCCCATCA 240  
QY 247 AGGTTCAGCGAGTGGATCTGGGACAGAGTTCACTCTCACCGCTGACAGCCCTGACAGCT 306  
Db 241 AGGTTCAGTGGCGGTGATCTGGGACAGATTTCATCTCCATCAACAGTCTGCAACCT 300  
QY 307 GAAGATTTTCCACTATATCTCTACAGGTTATAGTACCCCTGGAGCTGGGCCCA 366  
Db 301 GAAGATTTTCCACTATATCTCTACAGGTTATAGTACCCCTGGAGCTGGGCCCA 360  
QY 367 GGGACCAAGGTGGAAATCAAA 387  
Db 361 GGGACCAAGGTGGAAATCAAA 381

## RESULT 12

US-08-635-878-16

Sequence 16, Application US/08635878

Patent No. 5955364

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter  
APPLICANT: CHAMAT, Soulaïma Salim  
APPLICANT: PAN, Li-Zhen  
APPLICANT: WALSH, Edward E.  
APPLICANT: HEARD, Cheryl Janne  
APPLICANT: NEWMAN, Roland Anthony  
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN  
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND  
NUMBER OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: P. O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22113-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/635,878  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/488,376  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-150  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620









GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:50:12 : Search time 2581.68 Seconds  
(without alignments)  
3331.477 Million cell updates/sec

Title: US-09-019-441-4

Perfect score: 411  
Sequence: 1 ATGGAGTTGGCTGACCTG.....TCTGTGTCACCGTCTCTCA 411

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*  
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2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
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10: gb\_ro:\*  
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15: em\_da:\*  
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27: em\_sts:\*  
28: em\_un:\*  
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30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	289.8	70.5	405	9	HUMIGHADC	L06912 Human Ig re
2	283.6	69.0	437	9	HUMIGHVAK	M18513 Human (feta
3	279.4	68.0	415	9	HSBEL20	X81725 H.sapiens r
4	278.6	67.8	411	9	HSBEL28	X81726 H.sapiens r
5	277.4	67.5	417	9	HSBEL34	X81729 H.sapiens r
6	276	67.2	423	9	AF062285	AF062285 Homo sapi
7	275.8	67.1	402	9	AF062260	AF062260 Homo sapi
8	275.4	67.0	408	9	HSVHIC10	AJ234277 Homo sapi
9	275.2	67.0	470	9	HUMIGHCXE	M34024 Human fetal
10	274	66.7	470	9	HSB234278	AJ234278 Homo sapi
11	273.8	66.6	411	9	HSE5433	Z14201 H.sapiens r
12	273.8	66.6	437	9	HSIGHX13	X65895 H.sapiens m
13	272.8	66.4	420	9	HSBEL56	X81734 H.sapiens r
14	272.4	66.3	417	9	HSB234298	AJ234298 Homo sapi
15	272.4	66.3	414	9	AF062269	AF062269 Homo sapi
16	272.4	66.3	417	9	AF062269	AF062269 Homo sapi
17	271.2	66.0	423	9	AF062211	AF062211 Homo sapi
18	270.4	65.8	463	9	AF173920	AF173920 Macaca mu
19	270	65.7	441	9	HSR0U221	X81751 H.sapiens r
20	269.8	65.6	426	9	AF062206	AF062206 Homo sapi
21	269.8	65.6	463	9	AF173919	AF173919 Macaca mu
22	269.6	65.6	420	9	HSIGHXX18	X65900 H.sapiens m
23	269.6	65.6	423	9	AF062205	AF062205 Homo sapi
24	269.6	65.6	423	9	AF174012	AF174012 Homo sapi
25	269.2	65.5	448	9	HSE5434	Z14202 H.sapiens r
26	268.4	65.3	487	9	HSIG487	X61013 Human Immun
27	268.4	65.3	488	9	HSIG488	X61014 Human Immun
28	268.2	65.3	423	9	HSR0U10	X81736 H.sapiens r
29	268.2	65.3	463	9	AF173918	AF173918 Macaca mu
30	268	65.2	417	9	AF062276	AF062276 Homo sapi
31	267.4	65.1	411	6	BD004423	BD004423 Ameliorat
32	267.4	65.1	411	6	BD004479	BD004479 Therapeut
33	267.4	65.1	411	6	BD004540	BD004540 Therapeut
34	267.4	65.1	411	6	BD008373	BD008373 Inhibitin
35	267.4	65.1	411	6	E23343	E23343 Antibody ag
36	267.4	65.1	411	6	E27112	E27112 Remedy for
37	266.8	64.9	429	9	AF062182	AF062182 Homo sapi
38	266.8	64.9	429	9	AF062184	AF062184 Homo sapi
39	266.8	64.9	435	9	HSB234196	AJ234196 Homo sapi
40	266.4	64.8	426	9	HSR0U18	X81749 H.sapiens r
41	266.4	64.8	461	9	HSE54310	Z14200 H.sapiens r
42	266	64.7	450	9	HSU24080	U24080 Human Immun
43	265.8	64.7	437	9	HSE5435	Z14203 H.sapiens r
44	265.8	64.7	455	9	HUMIGHZM	L33852 Human Immun
45	265.6	64.6	486	9	HSIG486	X61011 Human Immun

## ALIGNMENTS

RESULT 1  
LOCUS HUMIGHADC 405 bp mRNA linear PRI 09-NOV-1994  
DEFINITION Human Ig rearranged gamma-chain mRNA V-region, 5' end of cds (from clone STIP15).  
ACCESSION L06912  
VERSION L06912.1 GI:185008  
KEYWORDS V-region; immunoglobulin gamma-chain; immunoglobulin heavy chain; processed gene.  
SOURCE Homo sapiens (tissue library: BC) Female Adult Synovium CDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 405)  
AUTHORS Bridges, S.L., Jr., Lee, S.K., Koopman, W.J. and Schroeder, H.W., Jr.  
TITLE Analysis of immunoglobulin gamma heavy chain expression in synovial tissue of a patient with rheumatoid arthritis  
JOURNAL Arthritis Rheum. 36 (5), 631-641 (1993)  
MEDLINE 93256941  
FEATURES Location/Qualifiers  
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Matches 343; Conservative 0; Mismatches 62; Indels 6; Gaps 1;

QY      1  ATGGAGTTTGGGCTGAGCTGGGTTTCCCTCTTCCTCTTTTGAAAGGTCCAGTGTAG 60
Db      1  ATGGAGTTTGGGCTGAGCTGGGTTTCCCTCTGTCTATTATPAAAGGTCCAGTGTAG 60

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Db      61  GTGCAGCTGTGTGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGTCCTGAGACTGTTC 120

QY      121  TGGCAGCTCTCCGGGTTTCAGTTCACCTTCAATAACTACTAGACTGGGTCCGCCAG 180
Db      121  TGTGCAGCTCTG-----GAATCACCTTTCAGTGTACTACTAGACTGGATCGGCCAG 174

QY      181  GCTCCAGGCGAAGGGGCTGGAGTGGGTCTCAGTATTATAGTAGTGTGATCCACATGG 240
Db      175  GCTCCAGGGAAGGGGCTGGAGTGGGTTTCAATCACTTACTCTACTAGCGGAATATCATATAC 234

QY      241  TACGACAGCTCCGTGAAGGCGAGATTTCACATCTCCAGAGAGAAGCCACATCAGACTG 300
Db      235  TACGACAGCTCTGTGAAGGCGCGATTTCACATCTCCAGAGGACAAAGCCAAAGACTCAGT 294

QY      301  TTTCTTCAATGAACAGCCTGAGAGCTGAGACACAGCGCTGTATTACTGTGCGAGCTTG 360
Db      295  TATCTCGAAATGAACAGCCTGAGAGCCGAGACACAGCGCATATATTACTGTGCGAGAGCG 354

QY      361  ACTACAGGCTGACTCTGTGGGGCCAGGGAATCCTGTGTACCGTCTCTCA 411
Db      355  GTTAGAGCGGGGCTACTGTGGGCGCAGGAAACCTGTGTACCGTCTCTCA 405

RESULT      2
LOCUS      HUMIGHVAK      437 bp      mRNA      linear      PRI 09-NOV-1994
DEFINITION      Human (fetal) rearranged Igm chain VDJ-region mRNA, clone 30PL.
ACCESSION      M18513
VERSION      M18513.1 GI:185539
KEYWORDS      C-region; D-region; J-region; V-region; immunoglobulin heavy chain;
              immunoglobulin mu-chain; processed gene; variable region subgroup
              VH-III.
SOURCE      Homo sapiens foetus liver cDNA to mRNA.
ORGANISM      Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 437)

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AUTHORS	Schroeder H.W. Jr., Hillson J.L. and Perlmutter R.M.
TITLE	Early restriction of the human antibody repertoire
JOURNAL	Science 238 (4828), 791-793 (1987)
COMMENT	8042812
MEDLINE	Draft entry and computer-readable sequence [1] kindly submitted by Schroeder 08-NOV-1988.
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Best Local Similarity	83.6%; Pred.No.4.2e-66;
Matches 351; Conservative	0; Mismatches 54; Indels 15; Gaps 2;
QY	1 ATGCAGTTTGGGCGAGCTGGGATTTCCTTCTCTTTTGAAGAAGTCCAGTGTAG 60
Db	24 ATGAGATTGGGCTAGCTGGCTTTTCTTTTGGGTATTAAAGAGTCCAGTGTAG 83
QY	61 GTGCAGCTGTGAGTGTGGGGGGGCTTGGCAAGCCTGGGGGGTCCCTGAGACTGTG 120
Db	84 GTGCAGCTGTGAGTGTGGGGGAGCTTGTGTACAGCTGGGGGGTCCCTGAGACTTCC 143
QY	121 TGGCAGGCTCCGGGTTACAGTTTCACTTCAATACACTCAATGAGTGGGTCCGCGAG 180
Db	144 TGTGAGGCTCTG-----GATTACCTTTAGCAGCTATGCTATGAGTGGGTCCGCGAG 197
QY	181 GCTCCAGGCGAGGGCTGAGTGGGTCCAGTATTAAGTATAGTAGTGGATCCCATGG 240
Db	198 GCTCCAGGGAAGGGGCTGAGTGGGTCTCAGCTATTAAGTATAGTGGTGTAGCAGATAC 257
QY	241 TACGACAGTCCGTTGAAGGGAGATTCACTTCATCCAGAGAAAGCCAGACACACTG 300
Db	258 TAGGAGACTCCGTTGAAGGGCGGTTCACTTCAGAGCAATTCAGAGACAGCTG 317
QY	301 TTTCTTCAATGAACAGCTGAGAGCTGAGACACAGGCTGTCTATTACTGTGCGA----- 355
Db	318 TATCTGCAATGAACAGCTGAGAGCCGAGACACAGGCGCTATATTACTGTGCGAAGAT 377



OY		356 --- -GCTTGACTACAGGGGTGCATCCCGTGGGGGCCAGGCAAGTCCTGTAACCGTCCTCCTCA	411
Dd	378	GCCCCGTGGGTTGCGGGTTTGACTACTACGGGGCCAGGAACCCTGTGCACCGCTCTCTCA	437
RESULT	3		
LOCUS	HSEBEL20	415 bp mRNA linear PRI 29-FEB-1996	
DEFINITION	H.sapiens rearranged VDJ region (HEL20).		
ACCESSION	X81725.1 GI:1212930		
KEYWORDS	diversity region; immunoglobulin heavy chain; joining region; variable region; VH-3 family.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
TITLE	Millil.M., Schiff.C., Fougereau M. and Tonnelle C. The VDJ repertoire expressed in human preB cells reflects the selection of bone fide heavy chains		
JOURNAL	Eur. J. Immunol. 26 (1), 63-69 (1996)		
MEDLINE	96152725		
REFERENCE	2 (bases 1 to 415) Tonnelle,C.		
AUTORS	Direct Submission		
JOURNAL	Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE		
COMMENT	Related sequences: X65741, X65883 to X65920.		
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	V-region	58..345	
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Dd	61 GTGCAAGCTGCTGAGTCTGGGGGCTTGSCAAAAGCTGGGGGTCCTGAGACTCTGG	120	
OY	121 TGCGAGCTCGCGGGTTCAGCTTTCACCTCATTAATACTAACATGACAGCGGTCCGCCAG	180	
Dd	121 TGCGAGCTCGCGGGTTCAGCTTTCACCTCATTAATACTAACATGACAGCGGTCCGCCAG	180	
OY	181 GCCTCAGGAGGAGGCTGAGTAGTGCTCACCTATTAGTAGTAGTAGTGATCCCACATGG	240	
Dd	175 CCTCAGGAGGAGGCTGAGTAGTGCTCACCTATTAGTAGTAGTAGTGATCCCACATGG	240	
OY	241 TAGCAGAAGCTCCGTGAGGAGGAGATTCACCATCTCCAGAGAGAGCCACAACACATGG	300	
Dd	241 TAGCAGAAGCTCCGTGAGGAGGAGATTCACCATCTCCAGAGAGAGCCACAACACATGG	300	

DB	235	TACGACAGCTCCGCTGAAGGGCCGAGTTACCACTTCTTCCAGACACACGCCAAGAACACTCACTG	294
QY	301	TTTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGCGCTGTCTATTACTGTGCGAGCTTG	360
DB	295	TATCTGCAAAATGAACAGCCTGAGAGCCGACGACAGCGCTGTTTATTACTGTCAAACTAG	354
QY	361	ACTA-----CAGGCTTGACTCTGGGGCCAGGAGATCCTGTGTCACCGTCTC	410
DB	355	AGGAAGTCCCGAGCTCTTTGACTACTGAGGGCCAGGAGAACCCGTCACACCTCTCCTC	414
QY	411	A	411
DB	415	A	415
RESULT	4		
LOCUS	HSBEL28	411 bp	mRNA
DEFINITION	H.sapiens rearranged VDJ region (BEL28).	linear	PRI 29-FEB-1996
ACCESSION	X81726		
VERSION	X81726.1	GI:1212931	
KEYWORDS	diversity region; immunoglobulin heavy chain; joining region; variable region; VH-3 family.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Euhayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 411)		
TITLE	Milli,M., Schiff,C., Fougereau,M. and Tonnelie,C.		
JOURNAL	The VDJ repertoire expressed in human preB cells reflects the selection of bone fide heavy chains		
MEDLINE	Eur. J. Immunol. 26 (1), 63-69 (1996)		
REFERENCE	96152725		
AUTHORS	2 (bases 1 to 411)		
TITLE	Tonnelie,C.		
JOURNAL	Direct Submission		
COMMENT	Submitted (15-SEP-1994) C. Tonnelie, Centre d'Immunologie		
FEATURES	Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE		
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	Matches 346; Conservative	0; Mismatches 59; Indels 12; Gaps 2;	
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DB	1	ATGGAGTTTGGGCTGAGCTGGGTTTCTTCTTGTGGCTATTTTAAAGGTCTCAAGTGTAG	60
QY	61	GTGCAAGCTGTGAGCTGTGGGGGCGGCTGTGCAAAAGCCTGGGGGTCCTGAGACTCTGG	120
DB	61	GTGCAAGCTGTGAGCTGTGGGGGAGGCTGTGTACACCTGGGGGGTCCCTGAGACTCTGC	120
QY	121	TGCGCAGCCTCCGGGTTTCAGTTTCACTTCAATACTACTACATGAGACTGGGTCCGCCAG	180

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 Oy 181 GCTCCAGGGAGGGGCTGGAGTGGGCTCTCAAGTATTAGTAGTGTGATGCCACATGG 240  
 Db 175 GCTCCAGGAGGAGGGGCTGGAGTGGGCTCTCAAGTATTAGTAGTGTGATGCCACATGG 234  
 Oy 241 TACGACAGCTCCGTGAAGGGCAGATTCCACCATCTCCAGAGAACGCAACACACTG 300  
 Db 235 TACGACAGCTCCGTGAAGGGGCTGGAGTGGGCTCTCAAGTATTAGTAGTGTGATGCCACATGG 294  
 Oy 301 TTTCTTAAATGAACAGCTCTGAGAGCTGAGACAGCGCTGTATTACTGTGG----- 354  
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 Oy 355 AGCTGTCACTGAGGCTGACTCTGGGGGCGAGGAGTCCGTGCTGACGCTCTCTCA 411  
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 LOCUS HSBEL34 417 bp mRNA linear PRI 29-FEB-1996  
 DEFINITION H.sapiens rearranged VDJ region (BEL34).  
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 VERSION X81729.1 GI:1212933  
 KEYWORDS diversity region; immunoglobulin heavy chain; joining region; variable region; VH-3 family.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 417)  
 AUTHORS M1111.M., Schiff,C., Fougereau,M. and Tonnellet,C.  
 TITLE The VDJ repertoire expressed in human preB cells reflects the selection of bone fide heavy chains  
 JOURNAL Eur. J. Immunol. 26 (1), 63-69 (1996)  
 MEDLINE 96152725  
 REFERENCE 2 (bases 1 to 417)  
 AUTHORS Tonnellet,C.  
 TITLE Direct Submision  
 JOURNAL Submitted (15-SEP-1994) C. Tonnellet, Centre d'Immunologie  
 COMMENT Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE  
 RELATED SEQUENCES: X65741, X65883 to X65920.  
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Query Match 67.5%; Score 277.4; DB 9; Length 417;  
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 Oy 409 TCA 411  
 Db 415 TCA 417

RESULT 6  
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 VERSION AF062285.1 GI:3171042  
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 SOURCE human.  
 ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 423)  
 AUTHORS Wang,X. and Stollner,B.D.  
 TITLE Immunoglobulin VH gene expression in human aging  
 JOURNAL Clin. Immunol. 93 (2), 132-142 (1999)  
 MEDLINE 99459182  
 JOURNAL PUBMED 10527689  
 REFERENCE 2 (bases 1 to 423)  
 AUTHORS Wang,X. and Stollner,B.D.  
 TITLE Direct Submision  
 JOURNAL Submitted (30-APR-1998) Biochemistry Department, Tufts University  
 COMMENT School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA  
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JOURNAL MEDLINE  
 Br. J. Haematol. 107 (3), 625-640 (1999)  
 REFERENCE 20050318  
 AUTHORS 2 (bases 1 to 411)  
 TITLE Noppe, S.M.  
 JOURNAL Direct Submission  
 Submitted (23-OCT-1998) Noppe S.M., Laboratory of Physiology, Free  
 University of Brussels Laarbeeklaan 103/E, 1090 Brussels, BELGIUM  
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 Best Local Similarity 82.5%; Pred. No. 6.9e-64;  
 Matches 344; Conservative 0; Mismatches 61; Indels 12; Gaps 2;  
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 Db 1 ATGAGATTGGGCGTGAAGTGGGTTTCCCTGTTCCCTTTTGAAGGTCGCCAGTGTGAG 60  
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 QY 181 GCTCCAGGAGGAGGCGTGGAGTGGTCTCAGCTATTAGTAGTAGTGATCC-----C 234  
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 DEFINITION H.sapiens mRNA for immunoglobulin heavy chain V-region (clone  
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 ACCESSION 247226  
 VERSION 247226.1 GI:1197316  
 KEYWORDS immunoglobulin; immunoglobulin heavy chain; variable region.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 113)  
 AUTHORS Demaison, C., David, D., Letourneur, F., Zouali, M., Saragostli, S. and  
 Theze, J.

TITLE	A cDNA/anchor-PCR approach to analyse the human VH gene repertoire expressed by peripheral CD19+ B cells reveals a strong bias usage		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 408)		
AUTHORS	Demaison,C.		
JOURNAL	Direct Submission		
TITLE	Submitted (16-DEC-1994) Christophe Demaison, Immunologie, Unite d'Immunogenetique Cellulaire-Institut Pasteur, 25, rue du docteur Roux, Paris, 75015, FRANCE		
REFERENCE	3 (bases 1 to 408)		
AUTHORS	Demaison,C., David,D., Letourneur,F., Theze,J., Saragosti,S. and Zouali,M.		
TITLE	Analysis of human VH gene repertoire expression in peripheral CD19+ B cells		
JOURNAL	Immunogenetics 42 (5), 342-352 (1995)		
MEDLINE	96006568		
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Db	1 ATGGAGTTTGGGCTGAGCTGAGCTGCTTTTCTTGTGGCTATTCTAAAGATGTCCAGTGTGAG 60		
Oy	61 GTGCACTGTGTGAGTCTGGGGGGCGCTTGGCAAAAGCCTGGGGGGTCCCTGAGACTGTGG 120		
Db	61 GTGCAAGCTGTGTGAGTCTGGGGGAGAGCTTGTGTAACAGCCGAGGGGGTCCCTGAGACTGTCC 120		
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Db	121 TGTGAGGCTCTG-----GATTACCTTTACACACTATGCCATGAGCTGGGTCCGCCAG 174		
Oy	181 GCTCCAGGCGAGGGGCTGGAGTGGGCTCTACACTATTAGTAGTAGTGTGATCCACATGG 240		
Db	175 GCTCCAGGGAAGGGGCTGGAGTGGGCTCTACAGTATTAGTAGTAGTGTGATCCACATAGC 234		
Oy	241 TACGAGAGACTCCGTAAAGGCGAGATTACACATCTCCAGAGAGAACGCCAACACACTG 300		
Db	235 TACGAGAGACTCCGTAAAGGCGGTTACACATCTCCAGAGAACAAATTCACAAAGACAGGTG 294		
Oy	301 TTTCTTCAATGAACAGCTTGAGACTGAGACACAGGCGTCTATTACTGTGCGAGCTTG 360		
Db	295 TATCTGCAATGAACAGGCTTGAGAGCCGAGGACACAGCCGCTATTACTGTGCGAAAGAT 354		
Oy	361 ACTACAGGCTC--TGACTCTGTGGGCGCAGGAGATCTGTGTACCGTCTCTCA 411		
Db	355 GGGCCCTTGACCCGAGACTACTGTGGGCGCAGGGAACCTGTGTCACGTCCTCTCA 408		
RESULT 10			
HUMIGHCXE	470 bp mRNA linear PRI 11-JUL-1995		
LOCUS	Human fetal Ig heavy chain variable region (clone M43) mRNA,		
DEFINITION	partial cds.		
ACCESSION	M34024		
VERSION	M34024.1 GI:185267		
KEYWORDS	D-region; J-region; V-region; immunoglobulin heavy chain; processed gene.		

SOURCE	Homo sapiens (individual isolate H8409) (clone: M43) 104 day foetus liver cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
AUTHORS	1 (bases 1 to 470)		
TITLE	Schroeder, H.W. Jr. and Wang, J.Y.		
JOURNAL	Preferential utilization of conserved immunoglobulin heavy chain variable gene segments during human fetal life		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 872 (1991), 6146-6150 (1990) 90349571		
COMMENT	Draft entry and computer-readable sequence for [Proc. Natl. Acad. Sci. U.S.A. (1990) In press] kindly submitted by H.W.Schroeder, Jr., 04-MAY-1990.		
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	/dev_stage="104 day fetus"		
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CDS	/gene="IGH"		
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Db	57 ATGAGATTGGGCTGAGCTGGGGTTTCCCTTGCTCTTTTGAAGGCTCCAGTGTAG 116		
OY	61 GTGCAGCTGTGTGACTGTGGGGCGGCTTGTGCAAGCCGTGGGGGCTCCCTGAGACTTGG 120		
Db	117 GTGCAGCTGTGTGAGTGTGGGGGAGGCTTGTGACAGCCGTGGGGGCTCCCTGAGACTTCC 176		
OY	121 TGGCAGCTCCGGGTTAGGTTCACCTTCATTAACCTCTACATGAGCTGGTCCGCCAG 180		
Db	177 TGTGCAAGCTCTG-----GATTCACCTTTTAGCACCTATGTCATGATGCTGGTCCGCCAG 230		
OY	181 GCTCCAGGCGAGGGCTGGAGTGGGCTCAGATTAATTAAGTAGAGTGATGCCACATGG 240		
Db	231 GCTCCAGGGAAGGGCTGAGTGGGCTCTCAGCTATTAGTGTGAGTGGTACACATAC 290		
OY	241 TACGAGACTCCGTGAAGGCGAGATTCAACATCTTCCAGAGAGAACGCCAACACACTG 300		
Db	291 TACGAGACTCCGTGAAGGCGGCTTACACCATCTCCAGACAAATTCAGAACACAGCTG 350		
OY	301 TTCTTCAATGACAGCTTGAGAGCTGAGGACACGCTGTCTATTACTGTGCGA----- 355		

Db	351	TATCTGCAAATGAAGAACAGCCTTGAGACCCGAGACACAGCGCCGATATATTACTGTGCGCAAAAAG	410
OY	356	---GCTTGACTACAGGGTCTGACTCTGTGAGGCGCAGGAGAGTCTGTGTCACGGTCTCTCA	411
Db	411	GACTGGAACGACACACTGGTTCGACCCCTGGGGCCAGGGAACCTGTGTCACGCTCTCTCA	470
RESULT	11		
LOCUS	HSA234278	411 bp	DNA linear PRI 10-DEC-1999
DEFINITION	HSA234278		
ACCESSION	AJ234278		
VERSION	AJ234278.1	GI:3821218	
KEYWORDS	heavy chain; immunoglobulin superfamily; variable region.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.		
AUTHORS	1 (bases 1 to 411)		
TITLE	Noppe,S.M., Heltman,C., Bakkus,M.H., Brissinck,J., Schots,R. and Thielemans,K.		
JOURNAL	The genetic variability of the VH genes in follicular Lymphoma: the impact of the hypermutation mechanism		
MEDLINE	Br J Haematol. 107 (3), 625-640 (1999)		
REFERENCE	20050318		
AUTHORS	2 (bases 1 to 411)		
TITLE	Noppe,S.M.		
JOURNAL	Submitted (23-OCT-1998) Noppe S.M., Laboratory of Physiology, Free University of Brussels Laarbeeklaan 103/E, 1090 Brussels, BELGIUM		
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	/clone="C9"		
	/cell_type="follicular lymphoma"		
gene	1..411		
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V_region	<1..>411		
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Best Local Similarity	82.3%; Pred. No. 1.9e-63;		
Matches 343; Conservative 0; Mismatches 62; Indels 12; Gaps 2;			
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Db	1	ATGGAGTTTGGGCTGAGCTGGCTTTTCTTGTCTATTAAAGGTGTCAGTGTAG	60
OY	61	GTGCACTGTGAGATGTGGGGGCGGCTTGGCAAAAGCCTGGGGGTCCTGAGACTGTGG	120
Db	61	GTGCAAGCTGTGAGATCTGGAAGAGGCTTGATCCAGCCTGGGGGTCCTGAGACTCTCC	120
OY	121	TGCGCAGCCTCGGGTTGAGTTCACCTTCAATAACTACTACATGAGACTGGTCGCCAG	180
Db	121	TGTGAGACCTCTG-----GGCTCACGCTCAGTAGCAGCTACATGAGCTGGTCCGACAG	174
OY	181	GCTCAGGGGACAGGGCTGTGAGTGGTCTCAGCTATTAGTAGTGGTATGC-----C	234
Db	175	GCTCCAGGGAAGGGGCTGAGTGGTCTCAGCTATTATTATGTGTGGAAACACATATTAC	234
OY	235	ACATGTACGAGAGATCCGTGAAGGGCAGATTACACATCTCAGAGAGAACCAACAC	294
Db	235	GCATCTACGAGAGATCCGTGAAGGGCAGATTACACATCTCAGAGAGAACATTTCCAGAC	294
OY	295	ACACGTGTTCTTCAATATACAGCCTGAGACTGAGACACAGGCTGTCTATTACTGTGCG	354

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Db      295  ACACATATATCTTCAATGAGACACCCCTGACAGTGAGAGACAGCCGATATTTACTGTGCG 354
OY      355  AGATTGACACGAGGCTGACTCTGGGGCCAGGAGTCTGGTCCACCGTCTCTCA 411
Db      355  AGATTGAGAGAGTGCCCTTGACGTCTGGGGCCAGGAGGACCGGTACCGTCTCTCA 411

RESULT  12
LOCUS    HSE5433                      437 bp    mRNA    linear    PRI 15-MAR-1993
DEFINITION H.sapiens rearranged Ig heavy chain variable region (VDJ).
ACCESSION Z14201 X65741
VERSION   2.14201.1 GI:30961
KEYWORDS  Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Ig variable region; immunoglobulin.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 437)
AUTHORS   Tonnelle,C.
TITLE     Direct Submission
JOURNAL   Submitted (09-JUN-1992) C. Tonnelle, Centre d'Immunologie
          Marseille-Luminy Case 906, 13288 Marseille Cedex 9, FRANCE
REFERENCE 2 (bases 1 to 437)
AUTHORS   Cuisinier,A.M., Gauthier,L., Boubill,L., Fougereau,M. and Tonnelle,C.
TITLE     Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in fetal liver
JOURNAL   Eur. J. Immunol. 23 (1), 110-118 (1993)
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                   36..>437
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BASE COUNT  93 a 104 c 136 g 104 t
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Best Local Similarity 82.7%; Pred. No. 1.9e-63;
Matches 340; Conservative 0; Mismatches 62; Indels 9; Gaps 2;

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OY      181  GCTCCAGGAGGAGGGCTGGAGTGGTCTCAGCATTAATAGTAGTGTGATCCCAATGG 240
Db      210  GCTCCAGGAGGAGGGCTGGAGTGGTCTCAGCATTAATAGTAGTGTGATCCCAATAG 269
OY      241  TACGACACTCCGCTGAAGGCGACATTCACCATCTCCAGAGAGAACCCCAACACACTG 300
Db      270  TACTCAGACTCCGCTGAAGGCGCGCTCACCATCTCCAGAGACATTCGAAGAACAGCTG 329
OY      301  TTTCTTCAATTAAGACAGCCTGAGAGCTGAGACACGCGTGTCTATTACTGTGCGACTTG 360
Db      330  TATCTCAATTAAGACAGCCTGAGAGCGGAGACACGCGTGTATTACTGTGCGACATAC 389
OY      361  ACTACAGGCTGACCTCGGGGCGAGGGAGTCCGTGACCGTCTCTCA 411
Db      390  ---CGGATCTTACACTAGTGGGCGCAGGAGACCTGTGTACCGTCTCTCA 437

RESULT  13
LOCUS    HSIGHXX13                      420 bp    mRNA    linear    PRI 26-JUL-1997
DEFINITION H.sapiens mRNA for XLA Ig heavy chain VDJ region (LE 3-12).
ACCESSION X65895 S58681
VERSION   2.65895.1 GI:395092
KEYWORDS  diversity region; Ig heavy chain; immunoglobulin; joining region; variable region.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 420)
AUTHORS   Schiff,C.
TITLE     Direct Submission
JOURNAL   Submitted (08-APR-1992) C. Schiff, Centre d'Immunologie de
          Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE
REFERENCE 2 (bases 1 to 420)
AUTHORS   Milla,M., Le Delst,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.
TITLE     Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire
JOURNAL   J. Clin. Invest. 91 (4), 1616-1629 (1993)
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Best Local Similarity 81.7%; Pred. No. 3.5e-63;
Matches 348; Conservative 0; Mismatches 57; Indels 21; Gaps 2;

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:06:57 ; Search time 3874.81 Seconds

(without alignments)  
1431.618 Million cell updates/sec

Title: us-09-019-441-4

Perfect score: 411  
Sequence: 1 ATGGAGTTTGCGCTGACGCTG.....TCTGTGTCACCGCTCTCTCA 411

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pin:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	69.1	406	9	AM401971 UI-HF-BKO
2	278.4	67.7	613	10	BM007475 603616742
3	277.2	67.4	511	9	AM402613 UI-HF-BKO
4	276	67.2	1164	10	BF974771 602245420
5	275.4	67.0	447	9	AM402793 UI-HF-BKO
6	272.8	66.4	471	9	AM403220 UI-HF-BKO
7	269	65.5	456	9	AM403059 UI-HF-BKO
8	269	65.5	582	9	AM401386 UI-HF-BKO
9	267.8	65.2	443	9	AM401428 UI-HF-BKO
10	266.8	64.9	440	9	AM408304 UI-HF-BKO
11	265.2	64.5	467	9	AM403862 UI-HF-BKO
12	265.2	64.5	740	10	BG75947 602714983
13	265.2	64.5	741	10	BG754024 602709552
14	264.2	64.3	510	9	AM403707 UI-HF-BKO
15	262.4	63.8	908	10	BG686881 602650867
16	262	63.7	879	10	BG759748 602711146
17	261.4	63.6	894	10	BG684839 602636557

18	261.2	63.6	840	10	BG756031 602716521
19	261	63.5	475	9	AM402740
20	260.8	63.5	587	10	BG684792 602636494
21	260.4	63.4	669	10	BG686716 602650678
22	258.8	63.0	411	9	AM403298
23	257.8	62.7	390	9	AM631411
24	257.8	62.7	397	9	AM403886
25	257.2	62.6	735	10	BG745292 602723604
26	257	62.5	613	10	BM007656 603617080
27	256.8	62.5	445	9	AM408316 UI-HF-BKO
28	256.6	62.4	768	10	BM007974 603617710
29	256.4	62.4	770	10	BG758713 602712981
30	255	62.0	491	9	AM402907 UI-HF-BKO
31	254.6	61.9	440	10	BG760171 602733261
32	254.6	61.9	483	9	AM402331 UI-HF-BKO
33	254.2	61.8	390	9	AM408285 UI-HF-BKO
34	254.2	61.8	412	9	AM402895 UI-HF-BKO
35	254	61.8	361	9	AM403412 UI-HF-BKO
36	254	61.8	823	10	BG547512 602574945
37	253	61.6	792	10	BF129047 601811377
38	252.8	61.5	648	10	BG340670 602462250
39	252.6	61.5	705	10	BG758682 602712929
40	252.6	61.5	735	9	AL551886 AL551886
41	251.8	61.3	548	9	AM408295 UI-HF-BKO
42	251.6	61.2	436	9	AM402311 UI-HF-BKO
43	251.4	61.2	372	9	AA581192 m338b11.1
44	250.8	61.0	870	10	BG684039 602635646
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#### ALIGNMENTS

RESULT 1  
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DEFINITION UI-HF-BKO-aao-c-04-0-UI.r1 NIH\_MGC\_36 Homo sapiens CDNA clone  
IMAGE:3054342 5', mRNA sequence.

ACCESSION AM401971 GI:6920657  
VERSION AM401971  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
1 (bases 1 to 406)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgapbs-femail.nih.gov](mailto:cgapbs-femail.nih.gov)  
Bco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/dbdp/image/image.html](http://www.bio.llnl.gov/dbdp/image/image.html)  
Seq primer: m3 forward

#### FEATURES

##### source

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/lab\_host="DH10B (LT1)"  
/note="Vector: p773-Pec; Site1: NotI; Site2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(0.5-1.5kb). Directionally cloned. Cells provided by Louis

BASE COUNT	89 a	93 c	123 g	100 t	1 others
ORIGIN	M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."				

Query Match	69.1%;	Score 284;	DB 9;	Length 406;
Best Local Similarity	82.5%;	Pred. No. 3.3e-68;		
Matches 339;	Conservative 0;	Mismatches 66;	Indels 6;	Gaps 1;

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 Db 2 ACGAGCTTGGGGGCTGTCTGGGTTTCCCTGTTTCAATTTTGAAGGTCGTCAGGTGTAG 61  
 QY 61 GTGCAGCTGTGTGAGTCTGTGGGGGGCGGCTTGGCAAAAGCTGGGGGGTCCCTGAGACTGTGG 120  
 Db 62 GTGCAGCTGTGTGAGTCTGTGGGGGAGGCTTGGACAGCTGGAGGGTCCCTGAGACTGTCC 121  
 QY 121 TGGCAGGCTCTCGGGGTTACGGTTACCTTTCATTACTACTACATGAGACTGGGTCCGCCAG 180  
 Db 122 TGTGCAAGCTCTG-----GATTCACCTTCAGTAATTTGAAATTAACGTGGGTCCGCCAG 175  
 QY 181 GCTCCAGGGGAGGGGCTGGAGTGGGTCCAGATTTATAGTAGAGGATGCCACATGG 240  
 Db 176 GCTCCAGGGGAGGGGCTGGAGTGGGTTCATACATTAATAGTAGAGGTAGTACCTATPAC 235  
 QY 241 TACGACAGCTCCGTGAAGGGCAGATTCCATCTTCCACAGAGAAGGCCAACACACTGTG 300  
 Db 236 TACGACAGCTCTGTGAAGGGCGAATTCCACATCTCCAGACAAAGCCNAGACACTGACTG 295  
 QY 301 TTTCTTCAATGAACAGGCTGAGAGCTGAGACACAGCGCTGTCTATTACTGTGCGAGCTTG 360  
 Db 296 TATGTGCAAAAGAACAGGCTGAGAGGCCAGGACACAGGCTGTTTATTACTGTGCGAGTCAA 355  
 QY 361 ACATAGAGGTGACTCTCTGGGGCAGGAGATCCGTGTACACGCTGCTCTCA 411  
 Db 356 TATTAAACAACAGCTGTACTGTGGGCCAGGGAACCCGTGGTACCGTCTCTCA 406

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EST 30-OCT-2001	
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BM007475	
BM007475.1	GI:16521829
EST.	
human.	
Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
1 (bases 1 to 613)	
NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .	
National Institutes of Health, Mammalian Gene Collection (MGC)	
Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>	
Tissue Procurement: Dr. Mark Watson	
cDNA Library Preparation: Ling Hong/Rubin Laboratory	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)	
DNA Sequencing by: Incyte Genomics, Inc.	
Clone distribution: MGC clone distribution information can be	
found through the I.M.A.G.E. Consortium/LNL at:	
<a href="http://image.lnl.gov">http://image.lnl.gov</a>	
Plate: LNC913	row: d column: 12
High quality sequence stop: 608.	

**FEATURES**

**SOURCE**

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BASE COUNT      126 a      172 c      174 g      141 t
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/Note="Organ: spleen; Vector: pOT7; Site1: XhoI; Site2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCGCGAG(g). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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Query Match	67.7%	Score	278.4;	DB	10;	Length	613;
Best Local Similarity	83.1%;	Pred. No.	1.3e-66;				
Matches	344;	Conservative	0;	Mismatches	61;	Indels	9;
				Gaps			2;

OY	1	ATGGAGTTTGGGGCTAGCGGGTTTTCCGTTGCTCTCTTTGAAAGGTCCTCAGTGTAG	60
Db	64	ATGGACACTGGGGCTTCGGCTGGGTTTCCCTGTGCTATTATTTGAAGAGTCTCCAGTGTGAG	123
OY	61	GTGCACTGATGAGACTGTGGGGGCGGCTTGGCAAGACCTGGGGGGTCCCTGAGACTGTG	120
Db	124	GTGCACTGTGTGAGACTGTGGGGGAGGCGCTGGTCAAGCTGTGGGGGGTCCCTGAGACTCTCC	183
OY	121	TGCGCAGCCTCCGGGTTGAGGTTCACTTCAATTAATCTACTACATGACTGGTCCGCCAG	180
Db	184	TGTGAGGCTCTG-----GAATCACCTTTCAGTAATCTAATACGTAACTGGCTCCGCCAG	237
OY	181	GCTCCAGGGCAGGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTGGTATCCCAATATG	240
Db	238	GCTCCAGGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTAGTAGTGGTATATAC	297
OY	241	TACGACAGATCCGTTGAAGGGCAGATTTCACCATCTCTCAGAGAGAACGCCAACAACACTG	300
Db	298	TACGACAGATCAGTGAAGAGGGCGAATTTCACCAATCTCCAGAGAACGCCAAGAATCTCAGT	357
OY	301	TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACAGGCTGTCTATTACTGTGCGAG--C	357
Db	358	TGGCTGCAAAATGAACAGCCTGAGAGCCGACAGGACAGGCTGTTTATTACTGTGTGAGGGCC	417
OY	358	TTGACGTACAGGGGTGACTCTGGGGGCCAGGAGATCTGTCACGCTCCCTCA	411
Db	418	CAGGATGGTTTCTTCGACTACTGGGGCCAGGAGGCTCTGGTACCGTCTCTCA	471

[illegible]

Cloned distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/dbrrp/image/image.html](http://www.bio.llnl.gov/dbrrp/image/image.html)  
Seq primer: M13 Forward.  
Location/Qualifiers

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source
1.511
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LT1)"
/notes="Vector: pTR73-Pac; Site.1: NotI; Site.2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT      104 a      131 c      151 g      125 t
ORIGIN

Query Match      67.4%; Score 277.2; DB 9; Length 511;
Best Local Similarity 82.6%; Pred. No. 2,7e-66;
Matches 347; Conservative 0; Mismatches 58; Indels 15; Gaps 2;

QY 1 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTTTTGAAGGTGCCAGTGGAG 60
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DB 14 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTTTTGAAGGTGCCAGTGGAG 73

QY 61 GTGCAGCTGTGAGTCTGGGGGCGCTTGCAAGGCTGGGCTCCAGACTCTGG 120
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 74 GTGCAGCTGTGAGTCTGGGGGCGCTTGCAAGGCTGGGCTCCAGACTCTCC 133

QY 121 TGGCAGACCTCCGGGTTTCAGGTTACCTTAATTAATTAATTAATTAATTA 180
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 134 TGTGTAGCCCTCTG-----GATTCACCTTATAGTATATAATTAATTAATTA 187

QY 181 GCTCCAGGAGGGGCTGAGTGGGCTGCTCAGTATTAATTAATTAATTAATTA 240
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 188 GCTCCAGGAGGGGCTGAGTGGGCTGCTCAGTATTAATTAATTAATTAATTA 247

QY 241 TAGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCAACACACTG 300
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 248 TAGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGAACGCAACACTG 307

QY 301 TTCTTCAATGAACAGCTGAGAGTACAGACAGGCTGTCTATTACTGTGGAGCTTG 360
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 308 TATCTGCAATGAACAGCTGAGAGTACAGACAGGCTGTCTATTACTGTGGAGACTC 367

QY 361 ACTAGAGG-----TCGACTCCTGGGGCCAGGAGAGGCTGGGACCGTCCCTCA 411
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 368 AATAGTGGAGTACTTTTGTGACTGTGGGCCAGGAGGAGGCTGGTCCCTCA 427

RESULT 4
BF974771      1164 bp      mRNA      linear      EST 22-JAN-2001
LOCUS
DEFINITION    602245420F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:433634 5',
                mRNA sequence.
ACCESSION     BF974771
VERSION       BF974771.1
KEYWORDS      GI:12341986
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE     1 (bases 1 to 1164)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
                Email: cgabbs-r@mail.nih.gov
                Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                CDNA Library Preparation: Ling Hong/Rubin Laboratory
                CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA Sequencing by: Incyte Genomics, Inc.

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FEATURES
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1.1164
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/db_xref="taxon:9606"
/clone="IMAGE:433634"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pORF7; Site.1: XhoI;
Site.2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the Laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

BASE COUNT      284 a      313 c      330 g      236 t      1 others
ORIGIN

Query Match      67.2%; Score 276; DB 10; Length 1164;
Best Local Similarity 82.2%; Pred. No. 7,6e-66;
Matches 350; Conservative 0; Mismatches 55; Indels 21; Gaps 2;

QY 1 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTTTTGAAGGTGCCAGTGGAG 60
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DB 64 ATGAGTTGGGCTGAGCTGGGTTTCTGTCCTTTTGAAGGTGCCAGTGGAG 123

QY 61 GTGCAGCTGTGAGTCTGGGGGCGCTTGCAAGGCTGGGCTCCAGACTCTGG 120
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 124 GTGCAGCTGTGAGTCTGGGGGCGCTTGCAAGGCTGGGCTCCAGACTCTCC 183

QY 121 TGGCAGACCTCCGGGTTTCAGGTTACCTTAATTAATTAATTAATTAATTA 180
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 184 TGTGTAGCCCTCTG-----GATTCACCTTATAGTATATAATTAATTAATTA 237

QY 181 GCTCCAGGAGGGGCTGAGTGGGCTGCTCAGTATTAATTAATTAATTAATTA 240
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 238 GCTCCAGGAGGGGCTGAGTGGGCTGCTCAGTATTAATTAATTAATTAATTA 297

QY 241 TAGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCAACACTG 300
    ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 298 TAGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGAGAACGCAACACTG 357

QY 301 TTCTTCAATGAACAGCTGAGAGTACAGACAGGCTGTCTATTACTGTGGAG---- 356
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 358 TATCTGCAATGAACAGCTGAGAGTACAGACAGGCTGTCTATTACTGTGGAGAGAT 417

QY 357 -----CTGACTACAGGCTGACTCTGGGGCCAGGAGTCTGGTCACTGC 405
    || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 418 CAGAGAACCAACAGCTGTAGATTGTGACTACTGGGGCCAGGAGAACCTGCACCTC 477

QY 406 TCCCTCA 411
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DB 478 TCCCTCA 483

RESULT 5
AM402793      447 bp      mRNA      linear      EST 16-FEB-2000
LOCUS
DEFINITION    UT-HF-BKO-aag-a-05-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
                IMAGE:3054608 5', mRNA sequence.
ACCESSION     AM402793
VERSION       AM402793.1
KEYWORDS      GI:6921535
SOURCE        human.
ORGANISM      Homo sapiens

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QY	406	TCCTCA	411	
Db	433	TCCTCA	438	
RESULT	7			
AM403059				
LOCUS				
DEFINITION				
AM403059				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

AM403059 456 bp mRNA linear EST 16-FEB-2000  
 UN-HF-BK-aat-f-10-0-U1.r1 NIH-MGC\_36 Homo sapiens cDNA clone  
 IMAGE:3054090 5', mRNA sequence.  
 AM403059  
 AM403059.1 GI:6921885  
 EST.  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 456)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.

clone distribution: MGC clone distribution information can be found through the I.M.P.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/dbfp/image/image.html](http://www-bio.llnl.gov/dbfp/image/image.html)  
Seq primer: M13 Forward.

FEATURES	source	Location/Qualifiers
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		/db_xref="taxon:9606"
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		/clone_id="NH_MGC_36"
		/tissue_type="Lymph"
		/cell_type="germinal center B cells"
		/cell_line="MGC85"
		/lab_host="DH10B (LTR)"
		/note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI;
		Constructed from size fractionated cytoplasmic mRNA
		(0.5-1.5kb). Directionally cloned. Cells provided by Louis
		M. Staudt, Ph.D. Library preparation by Maria de Fatima
		Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT		103 a
ORIGIN		104 c 139 g 110 t

Query Match	65.5%	Score 269	DB 9	Length 456
Best Local Similarity	83.9%	Pred. No. 4,9e-64		
Matches 318	Conservative 0	Mismatches 55	Indels 6	Gaps 1
QY	1	ATGGAGTTTGGGCTGTAGCTGGGGTTTCCCTGTCTCCCTTTTGAAGGTCGTCCAGTGTGAG	60	
Db	52	ATGGAGTTGGGGGCTGTGCTGGGTTTCCCTGTTGTTTGAAGGTCGTCCAGTGTGAG	111	
QY	61	GTCGACGTGTGGAGATCTGGGGGGCGGCTTGGCAAAAGCCGGGGGGTCCCTGACATCTGG	120	
Db	112	GTGCAAGTGTGTGGAATCTGGGGGGAGGCTTGGTACAGCCTGGAGGGTCCCTGACATCTCC	171	
QY	121	TGCGCAGCTCCGGGGTTCAGGTTCACTTCAATTAACATACTACATGAGCTGGGTCCGCCAG	180	
Db	172	TGTGTGAGCCTCTG-----GATTCACTTCCTACGTAGTATTGAAATAACCTGGGTCCGCCAG	225	
QY	181	GCTCCAGGCGAGGGGCTGGAGTGGTCCACAGTTATAGTAGAGTGGATGCCACATATC	240	
Db	226	GCTCCAGGGAAGGGGCTGTGAGTGGTTTCATACATTAAGTAGTAGTGTGTATACCATATAC	285	
QY	241	TACGCAGATCCGTGAAGGGCAGATTTCACATCTCCAGAGAGAGCCCAACAACACTGT	300	

Accession	Sequence	Position
Db	TACGACACTCTGTGAAGGGCCGATTCACATCTCCAGAGACCAACGCCAAGAACTCACTG	345
Qy	TTTCTTAAATGAACAGCCGAGAGCTGAGAGACACGGCTGTATATTACTGTGAGCTTG	360
Db	TATCTGAAATGAAGACCTGAGAGCCGAGAGACACGGCTTTATATTACTGTGAGGCAT	405
Qy	ACTACAGGTCCTGACTCCT	379
Db	ATAGCAGCAGCTGACGACT	424

RESULT	8	582 bp	mRNA	linear	EST 16-FEB-2000
LOCUS	AM401386				
DEFINITION	U1-HF-BKO-aau-b-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE3055324 5', mRNA sequence.				
ACCESSION	AM401386				
VERSION	AM401386.1	GI:6920168			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 582)	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.	Email: <a href="mailto:cgaps-r@mail.nih.gov">cgaps-r@mail.nih.gov</a>	Eco RI site shown at the beginning of the sequence.	
	Tissue Procurement: Louis M. Straud, M.D., Ph.D.	cdNA Library Preparation: M.B. Soares Lab	cdNA Library Arrayed by: M.B. Soares Lab	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://www.bio.lnl.gov/bbrp/image/image.html">www.bio.lnl.gov/bbrp/image/image.html</a>	Seq primer: M13 forward.		

FEATURES	SOURCE
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/clone="IMAGE:3055324"	
/clone_1b="NH_MGC_36"	
/tissue_type="lymph"	
/cell_type="germinal center B cells"	
/cell_line="MGC85"	
/lab_host="DH10B (L17)"	
/note="Vector: pRT3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."	
BASE COUNT	117 a 155 c 169 g 141 t
ORIGIN	

Query Match	65.5%	Score 269	DB 9	length 582
Best Local Similarity	81.5%	Pred. No. 5.3e-64		
Matches 340	Conservative	0	Mismatches 65	Indels 12
			Gaps	2
QY	1	ATGAGAGTTGGGCTGAGCTGGGTTTCCCTTCTCTTTGAAAGGTGTCACAGTGTGAG	60	
Db	75	ATGAGAGTTGGGCTGAGCTGGGTTTCCCTTCTCTTTGAAAGGTGTCACAGTGTGAG	134	
QY	61	GTGACAGTGTGAGTGTGAGGCGGCTTGGCAAAAGCTGGGGGGTCCCTGAGACTGG	120	
Db	135	GACATCTGTGTGAGATCTGGGGGAGCCCTTGGTACAGCCTGGAGGGTCCCTGAGACTTCC	194	
QY	121	TGGCAGAGCTCCGGGTTCCAGTTGACCTTCAATTAACACTACATGAGACTGGTCCGCCAG	180	
Db	195	TGTGTGAGGCTCTG-----GATTACACTTTCAGTGTATGTAATTCAGCTGGTCCGCCAG	248	

QY 181 GCTCCAGGCGAGGCGCTGAGTGGCTCAAGTATTAGTACTGCTGATCCACATGC 240  
 Db 249 GCTCCAGGCGAGGCGCTGAGTGGCTCAAGTATTAGTACTGCTGATCCACATGC 308  
 QY 241 TAGCAGACTCCGCTGAGGCGAGTTCACATCTCCAGAGAACGCCAACACACTG 300  
 Db 309 TAGCAGACTCCGCTGAGGCGAGTTCACATCTCCAGAGAACGCCAACACACTG 368  
 QY 301 TTCTCTCAATGAACAGCCTGAGAGCTGAGACAGCGCTCTATTACTGTGCG----- 354  
 Db 369 TTCTCTCAATGAACAGCCTGAGAGCTGAGACAGCGCTCTATTACTGTGCGAACGCT 428  
 QY 355 AGCTGACTACAGGCTGTGACTCTCTGGGCGCAGGAGTCTGTGACCTCTCTCTCA 411  
 Db 429 ATTTGACTGTAGCTTGTGACTCTGTGGGCGCAGGAGCCTGTGACCTCTCTCTCA 485

RESULT 9  
 AM401428 443 bp mRNA linear EST 16-FEB-2000  
 LOCUS UI-HF-BK0-aad-b-02-0-UI.r1 NIH\_MGC\_36 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3053139 5', mRNA sequence.  
 ACCESSION AM401428  
 VERSION AM401428.1 GI:6920011  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 443)  
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html  
 Seq primer: M13 forward.  
 Location/Qualifiers  
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 /tissue\_type="lymph"  
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 /cell\_line="MGC85"  
 /lab\_host="DH10B (LTI)"  
 /note="vector: pTV73-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 93 a 116 c 131 g 103 t  
 ORIGIN

Query Match 65.2% Score 267.8; DB 9; Length 443;  
 Best Local Similarity 81.1%; Pred. No. 1e-63; Indels 18; Gaps 2;  
 Matches 343; Conservative 0; Mismatches 62;

QY 1 AAGGACTTTGGGCTGAGTGGCTTTCTCTCTTTTGAAGGTGTCAGTGTGAG 60  
 Db 25 AAGGACTTTGGGCTGAGTGGCTTTCTCTCTTTTGAAGGTGTCAGTGTGAG 84  
 QY 61 GTGCAGCTGTGAGTGTGAGTGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTGC 120

Db 85 GTGCAGCTGTGAGTGTGAGTGGGCGCTTGGCAAGCCTGGGGGGTCCCTGAGACTCTCC 144  
 QY 121 TGGCAGCTTCGCGGTTGAGTTCACCTTCAATTAAGTACTGATGAGTCCGCGAG 180  
 Db 145 TGTGACACTCTG-----GATTCACCTTCAATTAAGTACTGATGAGTCCGCGAG 198  
 QY 181 GCTCCAGGCGAGGCGCTGAGTGGCTCAAGTATTAGTACTGCTGATCCACATGC 240  
 Db 199 GCTCCAGGCGAGGCGCTGAGTGGCTCAAGTATTAGTACTGCTGATCCACATGC 258  
 QY 241 TAGCAGACTCCGCTGAGGCGAGTTCACATCTCCAGAGAACGCCAACACACTG 300  
 Db 259 TAGCAGACTCCGCTGAGGCGAGTTCACATCTCCAGAGAACGCCAACACACTG 318  
 QY 301 TTCTCTCAATGAACAGCCTGAGAGCTGAGACAGCGCTCTATTACTGTGCGAGCTTG 360  
 Db 319 TTCTCTCAATGAACAGCCTGAGAGCTGAGACAGCGCTCTATTACTGTGCGAGAGCA 378  
 QY 361 ACTACAGG-----TGTACTCTGTGGGCGCAGGAGTCTGTGACCTCTCTC 408  
 Db 379 GTTCCCATGCTGAGTTCATTTGACTTGTGGGCGCAGGAGCCTGTGACCTCTCTC 438  
 QY 409 TCA 411  
 Db 439 TCA 441

RESULT 10  
 AM408304 440 bp mRNA linear EST 16-FEB-2000  
 LOCUS UI-HF-BK0-abj-e-10-0-UI.r1 NIH\_MGC\_36 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3056371 5', mRNA sequence.  
 ACCESSION AM408304  
 VERSION AM408304.1 GI:6927361  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 440)  
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/dbp/image/image.html  
 Seq primer: M13 forward.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3056371"  
 /clone\_1lb="NIH\_MGC\_36"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LTI)"  
 /note="vector: pTV73-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 99 a 98 c 134 g 109 t  
 ORIGIN





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/note="Organ: B-cells; Vector: pOTB7; Site_1: xhoI;  
Site_2: EcoRI; cDNA made by oligo-dT priming.
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/clone="IMAGE:3056391"  
/clone_lib="NIH_MGC_36"
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/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LR1)"
/Note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staedt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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BASE COUNT 110 a 137 c 149 g 114 t

ORIGIN

Query Match 64.3%; Score 264.2; DB 9; Length 510;  
Best Local Similarity 79.6%; Pred. No. 1.1e-62;  
Matches 327; Conservative 0; Mismatches 78; Indels 6; Gaps 1;

QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTCCTTTTGAAGGTGCCAGTGTGAG 60  
DB 38 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTCCTTTTGAAGGTGCCAGTGTGAG 97

QY 61 GTGCAGCTGTGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTGTGG 120  
DB 98 GTGCAGCTGTGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGTCCTGAGACTGTCC 157

QY 121 TGGCAGACCTCCGGGTTCAAGGTTACCTTCAATTACTACTACATGAGCTGGTCCGCGAG 180  
DB 158 TGTGCAGACTCTG-----GATTCACCTTTAGCAACATATCCATGAGCTGGTCCGCGAG 211

QY 181 GCTCCAGGGGAGGGGCTGGAGTGGGTCACGTAATAGTATGTGTGATCCACATGTG 240  
DB 212 GCTCCAGGGGAGGGGCTGGAGTGGGTCATATTAATTAATGCGAGATGATGATCCATTC 271

QY 241 TACGCACTCCGCTGAGAGGCGAGATTCACCATCTCCAGAGAGAACGCAACACACTG 300  
DB 272 TATGCACTCCGCTGAGAGGCGGTTTCCATCTCCAGATATATTCAGAGAACACTTG 331

QY 301 TTCTTCAATGAACACCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGGAGCTTG 360  
DB 332 TATCTGCAATGAACACCTGAGAGCGCGAGACACGCGCTTATATTACTGTGGAGAGCA 391

QY 361 ACTAGAGGCTCTGACTCTGGGGGAGAGTCTGTGTCACCGTCCTCA 411  
DB 392 GACTACGGTCCCTCTACTGGGCGAGGAACTGTGTCACCGTCTCTCA 442

RESULT 15 908 bp mRNA linear EST 01-MAY-2001  
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LOCUS 602650867F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4763153 5',  
DEFINITION mRNA sequence.  
ACCESSION BG686881  
VERSION BG686881.1 GI:13918278  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 908)  
NIH-MGC <http://imgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
<http://image.llnl.gov>  
Plate: LICM1618 row: f column: 18  
High quality sequence stop: 899.

FEATURES  
source Location/Qualifiers  
1. 908  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4763153"  
/clone\_lib="NIH\_MGC\_48"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/Note="Organ: B-cells; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCAAGAG(G). Size-selected  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the Laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH-MGC library." 2 others

BASE COUNT 200 a 262 c 250 g 194 t

ORIGIN

Query Match 63.8%; Score 262.4; DB 10; Length 908;  
Best Local Similarity 85.2%; Pred. No. 4.1e-62;  
Matches 306; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTCCTTTTGAAGGTGCCAGTGTGAG 60  
DB 71 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTCCTTTTGAAGGTGCCAGTGTGAG 130

QY 61 GTGCAGCTGTGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTGTGG 120  
DB 131 GTGCAGCTGTGAGTCTGGGGCGGCTTGGTACAGCCTGGGGGTCCTGAGACTGTCC 190

QY 121 TGGCAGACCTCCGGGTTCAAGGTTACCTTCAATTACTACTACATGAGCTGGTCCGCGAG 180  
DB 191 TGTGCAGACTCTG-----GATTCACCTTCAATAGTATGATGATGATCCATTC 244

QY 181 GCTCCAGGGGAGGGGCTGGAGTGGGTCACGTAATAGTATGTGTGATCCACATGTG 240  
DB 245 GCTCCAGGGGAGGGGCTGGAGTGGGTCATCCATTAATAGTATGATGATTCATATAC 304

QY 241 TACGCACTCCGCTGAGAGGCGAGATTCACCATCTCCAGAGAGAACGCAACACACTG 300  
DB 305 TACGCACTCCGCTGAGAGGCGGATTCACCATCTCCAGAGAGAACGCAACACTG 364

QY 301 TTCTTCAATGAACACCTGAGAGCTGAGAGACAGGCTGTCTATTACTGTGGAGCTT 359  
DB 365 TATCTGCAATGAACACCTGAGAGCGCGAGACAGGCTGTGATTAATCTGTGGAGGTT 423

Search completed: September 23, 2002, 17:07:01  
Job time: 4520 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:58:50 ; Search time 488.47 Seconds

(without alignments)  
1444.617 Million cell updates/sec

Title: us-09-019-441-4

Perfect score: 411  
Sequence: 1 ATGGAGTTTGGCGTGCAGCTG.....TCTGTGTCACGCTCTCTCA 411

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	369.4	89.9	19035	19	AAV61794
3	293	71.3	458	22	AAH41153
4	282.6	68.8	1710	22	AA522533
5	282.6	68.8	1721	22	AA522530
6	267.4	65.1	411	19	AAV24243
7	267.4	65.1	411	20	AAZ00116
8	267.4	65.1	411	21	AA258914
9	267.4	65.1	411	22	AAH75115

10	267.4	65.1	411	22	AAH74285	Nucleotide sequenc
11	267.4	65.1	411	22	AAH76645	Humanised anti-PTH
12	267.4	65.1	411	22	AAH69130	Human antibody H c
13	267.4	65.1	411	22	AAH69186	Human antibody H c
14	267.4	65.1	411	22	AAH69242	Human antibody H c
15	266	64.7	1458	22	AA522625	Human CDNA encodin
16	262.2	63.8	1983	22	AAH98583	Human EST-derived
17	261.6	63.6	1741	22	AA522531	Human EST-derived
18	261.2	63.6	1366	22	AAH98760	Human EST-derived
19	261	63.5	456	11	AAQ03610	Sequence encoding
20	260	63.3	1736	22	AA522532	Human CDNA encodin
21	259.6	63.2	1427	19	AAV41431	Plasmid Hui9CHPCP
22	258.2	62.8	432	15	AAQ71717	Monoclonal antilbod
23	258	62.8	1427	19	AAV41432	Plasmid Hui9CHPCP
24	258	62.8	1427	19	AAV41432	Plasmid Hui9CHPCP
25	256.8	62.5	637	23	AA591077	DNA encoding novel
26	256.6	62.4	445	18	AA772237	Humanised reshaped
27	254.6	61.9	1392	21	AAA46864	DNA encoding the h
28	254.6	61.9	1392	21	AAA46890	DNA encoding the h
29	254.6	61.9	1392	21	AAA46892	DNA encoding the h
30	254.6	61.9	1999	21	AAA46891	DNA encoding the h
31	253.2	61.6	1395	21	AAA46866	DNA encoding the h
32	253.2	61.6	1395	21	AAA46894	DNA encoding the h
33	252.6	61.5	1392	21	AAA46870	DNA encoding the h
34	252.6	61.5	1392	21	AAA46896	DNA encoding the h
35	252.2	61.4	393	17	AAH46130	Monoclonal antilbod
36	252.2	61.4	393	18	AAH85839	Monoclonal antilbod
37	252	61.3	1651	21	AAAI5694	Cancer suppressor
38	252	61.3	1651	22	AAQ07360	Human DNA encoding
39	251.8	61.3	483	13	AAQ31888	CLN-IgG gamma. SY
40	251.8	61.3	483	15	AAQ64065	Anti-cancer monoc
41	251.4	61.2	411	20	AA622787	Human anti-ganglio
42	251.2	61.1	761	20	AAH01214	Human antiFc epsil
43	250.8	61.0	1605	22	AAH18432	Human CDNA sequenc
44	250.6	61.0	393	15	AAQ64051	Sequence of the VH
45	247.6	60.2	1951	24	AA562797	CDNA sequence #584

#### ALIGNMENTS

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AAV33310	
ID	AAV33310 standard; DNA: 411 BP.
XX	
AC	AAV33310;
XX	
DT	18-NOV-1998 (first entry)
XX	
DE	Anti-human CD23 5E8 monoclonal antibody heavy chain variable region DNA.
XX	
KW	Anti-human CD23 5E8 monoclonal antibody; heavy chain variable region;
KW	human CD23; IGE: FcεR1/CD23; gamma-1 constant region;
KW	gamma-3 constant region; allergy; inflammation; autoimmune disease;
KW	allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
XX	
OS	Macaca fascicularis
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..411
FT	/tag a "anti-human CD23 5E8 heavy chain variable
FT	/product- "region"
FT	/note- "CDS does not contain a stop codon"
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FT	sig_peptide
FT	/tag- b
FT	58..411
FT	mat_peptide
FT	/tag- c
FT	148..168
FT	misc_feature
FT	/tag- d
FT	/note- "encodes CDR 1 region"
FT	211..261
FT	misc_feature
FT	/tag- e





Db 9672 tacgcagaccctcgtaaggcgagattaccacatctccagagagaacccaagaacacactg 9731  
 QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGCTGCTATTACTGTGCGAGCTTG 360  
 Db 9732 ttcttcaaatgaacagcccgagagcgcgagagacacagcgtctctattactgcgcgagcttg 9791  
 QY 361 ACTACAGGGTCTGACTCTCTGGGCGCCAGGGAGTCTCTGCTACCGCTCTCTCTCA 411  
 Db 9792 actacagggctgactcctctgggcccaggagctcctggttcacccgtctctctca 9842

RESULT 3  
 AAH41153  
 ID AAH41153 standard; DNA: 458 BP.  
 XX  
 AC AAH41153;  
 XX  
 DT 22-AUG-2001 (first entry)  
 DE  
 DE Human coding sequence SEQ ID 3.  
 XX  
 KW Human: antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;  
 KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;  
 KW signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200136642-A1.  
 XX  
 PD 25-MAY-2001.  
 XX  
 PF 17-NOV-2000; 2000WO-JP08129.  
 XX  
 PR 18-NOV-1999; 99JP-0328681.  
 PR 08-NOV-2000; 2000JP-0340216.  
 XX  
 PA (NISR) JAPAN TOBACCO INC.  
 XX  
 PI Sakamoto S, Kamada M;  
 XX  
 DR WPI: 2001-343825/36.  
 DR P-PSDB; AAB99111.  
 XX  
 PT Human monoclonal antibodies recognizing human TGF-beta II receptor,  
 PT useful for treating TGF-beta associated diseases such as tissue  
 PT fibrosis -  
 XX  
 PS Example 12; Page 94-95; 118pp; Japanese.  
 XX  
 CC The present invention relates to novel human monoclonal antibodies. The  
 CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II  
 CC receptor, resulting in the inhibition of the signal transduction of human  
 CC TGF-beta into cells. The antibodies can be used for the prevention and  
 CC treatment of diseases associated with the production of TGF-beta, such as  
 CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,  
 CC atherosclerosis, atopy, keloid and arthritis. The present sequence was  
 CC used in the present invention.  
 XX  
 XX Sequence 458 BP; 92 A; 121 C; 139 G; 106 T; 0 other;

Query Match 71.3%; Score 293; DB 22; Length 458;  
 Best Local Similarity 83.9%; Pred. No. 2.7e-73;  
 Matches 345; Conservative 0; Mismatches 60; Indels 6; Gaps 1;

QY 1 ATGAGCTTTGGGCTGAGCTGGGCTTTCTCTGTTCTCTTTTGAAGGTGTCAGTGTGAG 60  
 Db 1 atggaactgggctccgcgtgggtttccctgttctatttagaagggtcccaagtgtgag 60  
 QY 61 GTCAGCTGTGAGTCTGGGGCGGCTGGCAAGCTGGGGGTCCTGAGACTCTGG 120  
 Db 61 gtcaactggtagtctggggagggcctggttcaggcctgggggtccctgagactctcc 120

QY 121 TGCGCAGCCTCGGCTTCAGGTTCACTTCAATAACTACTACATGGACTGGTCCGCCAG 180  
 Db 121 tggcagcctcg-----gattcaccttcagtagcttttagcactgaactggtgccgccag 174  
 QY 181 GCTCCAGGGCAGGGGCTGAGTGGGTCTCAGCTATTAGTAGTAGTGTGATCCCATCG 240  
 Db 175 gtccagggaagggtggtgagtggtctccatcatagtagtagtagtagttacatatac 234  
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 Db 235 tacacagactcagtggaaggccgattcaccatctccagagacaacgccaaagaactcactg 294  
 QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACAGCGCTGCTATTACTGTGCGAGCTTG 360  
 Db 295 tatctgcaaatgaacagcctgagagccgagagacacagcgtgtattactgtgcgagagg 354  
 QY 361 ACTACAGGCTGACTCTCTGGGCGCCAGGGAGTCTCTGCTACCGCTCTCTCTCA 411  
 Db 355 tactgggggttgactactggggccagggaacctgtcacccgtctctctca 405

RESULT 4  
 AAS22533  
 ID AAS22533 standard; cDNA: 1710 BP.  
 XX  
 AC AAS22533;  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE  
 DE Human cDNA encoding a novel human protein #99.  
 XX  
 KW Human: novel protein; ss; Antianaemic; osteopathic; antiinflammatory;  
 KW immunomodulatory; cytostatic; neuroprotective; vulnary; nootropic;  
 KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
 KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
 KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
 KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
 KW tissue regeneration; immune disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200155437-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-US02623.  
 XX  
 PR 25-JAN-2000; 2000US-0491404.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI: 2001-451939/48.  
 DR P-PSDB; AAU14228.  
 XX  
 PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
 PT nervous system disorders, and for regenerating bone and cartilage -  
 XX  
 PS Claim 1; Page 306-308; 894pp; English.  
 XX  
 CC The invention relates to polynucleotides encoding novel human  
 CC proteins or their active domains. The polypeptides, polynucleotides and  
 CC antibodies raised against the polypeptides are used in a method of  
 CC treatment of a mammal and prevention of disorders caused by the aberrant  
 CC protein expression or activity. The polypeptides can be used as  
 CC molecular weight markers, food supplements, and in antibody production.  
 CC The polypeptides are used to identify compounds which bind to the  
 CC polypeptides. Polynucleotides of the invention are used as probes and  
 CC primers, for sequencing, for chromosome or gene mapping, in the  
 CC production of recombinant proteins, and in generating anti-sense DNA or  
 CC RNA and in gene therapy. Polypeptides of the invention can be used to  
 CC target drugs to a tumour. In assays to determine biological activity, to















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Q	y	361	ACTACAGGGTCTGAC-----TCCTGGGGCCAGGGAGTGCTCGTCAACCGTCTCCTCA	411
D	b	355	actactatgacttactttgcttacttggtggccaggaaacctggtcacctgttcctca	411
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X	X	AAF69242;		
X	X	17-APR-2001 (first entry)		
D	T	XX		
D	E	Human antibody H chain protein SEQ ID NO:58.		
X	X	Human; mouse; drug-resistant hyperglycaemia; PTHrP; cardiovascular;		
K	W	parathyroid hormone related peptide; gastrointestinal; cancer;		
K	W	central nervous system; calcium-antagonist; bone resorption inhibitor		
K	W	bisphosphonate; calcitonin; calcium elimination promoter;		
K	W	intestinal calcium absorption inhibitor; ds.		
X	X	Homo sapiens.		
O	S	XX		
P	N	WO200102012-A1.		
X	X	11-JAN-2001.		
P	D	XX		
X	X	06-JUL-2000; 2000WO-JP04523.		
P	F	XX		
X	X	06-JUL-1999; 99JP-0192270.		
P	R	XX		
X	X	(CHUS ) CHUGAI SEIYAKU KK.		
P	A	XX		
P	I	Saito H, Tsunenari T, Onuma E;		
X	X	WPI; 2001-123066/13.		
D	R	XX		
P	T	Agents inhibiting binding of parathyroid hormone related peptide to i		
P	T	receptor for treatment of drug-resistant hyperglycemia -		
X	X	Example; Page 95-96; 118pp; Japanese.		
P	S	XX		
C	C	The present invention describes an agent (I) for the treatment of		
C	C	drug-resistant hyperglycaemia. (I) contains as an active component a		
C	C	substance which inhibits the binding of parathyroid hormone related		
C	C	peptide (PTHrP) to its receptor. (I) is a calcium-antagonist. (I) can		
C	C	be used for treatment of drug-resistant hyperglycaemia e.g. associated		
C	C	with cancer. The hyperglycaemia is resistant to treatment with other		
C	C	drugs including bone resorption inhibitors (such as bisphosphonate or		
C	C	calcitonin), calcium elimination promoters and intestinal calcium		
C	C	absorption inhibitors. AAF69197 to AAF69252 and AAB76917 to AAB76935		
C	C	represent sequences used in the exemplification of the present		
C	C	invention.		
X	X	Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;		
S	Q			

Db	121	tgtycagcctctg-----gattcaccttccagtagcatggaatgtcttctgtgggtccgcag	174
Qy	181	GCTCAGGCGAGGGGTGGAGTGGGTCTCACGTATTAGTAGTGGTGATCCACATGG	240
Db	175	gctcaggcaagggtgagtggtggtgcacattagtggtggtgttacacctac	234
Qy	241	TACGCAGACTCCGTGAAGGCGAGATTCCACTCTCCAGAGAGAACGCCACACACATG	300
Db	235	tatccagacagtgtgaagggtgattccacattccagagacaattccaagaacacgtg	294
Qy	301	TTTCTTCAAATGAACAGCCTGACAGCTGAGGACAGCGGTGTCTATTACTGTGCGAGCTTG	360
Db	295	tatctgcaaatgaacagcctgagagctgagggacagcgtgtctattactgfcgagacag	354
Qy	361	ACTACAGGGTCTGAC-----TCTTGGGGCCAGGGAGTCTGTGTCACCGTCTCCCTCA	411
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XX	AC	AA522625;	
XX	DT	24-OCT-2001 (first entry)	
XX	DE	Human cDNA encoding a novel human protein #191.	
KW	Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory;		
KW	immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;		
KW	anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;		
KW	antibacterial; immunologic; dermatological; haemostatic; antiasthmatic;		
KW	thrombolytic; immunogen; antibody; gene therapy; neurological disorder;		
KW	Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis		
KW	tissue regeneration; immune disorder.		
OS	Homo sapiens.		
XX	PN	WO200155437-A2.	
XX	PD	02-AUG-2001.	
XX	PF	25-JAN-2001; 2001WO-0502623.	
XX	PR	25-JAN-2000; 2000US-0491404.	
XX	PA	(HYSE-) HYSEQ INC.	
XX	FI	Tang YT, Liu C, Drmanac RT;	
XX	DR	WPI: 2001-451939/48.	
XX	DR	P-PSDB; AAU14320.	
PT	PT	Isolated polypeptides useful for treating anti-inflammatory diseases,	
PT	PT	newborn system disorders, and for regenerating bone and cartilage -	
XX	PS	Claim 1; Page 432-434; 894pp; English.	
XX	CC	The invention relates to polynucleotides encoding novel human	
CC	CC	proteins or their active domains. The polypeptides, polynucleotides and	
CC	CC	antibodies raised against the polypeptides are used in a method of	
CC	CC	treatment of a mammal and prevention of disorders caused by the aberrant	
CC	CC	protein expression or activity. The polypeptides can be used as	
CC	CC	molecular weight markers, food supplements, and in antibody production.	
CC	CC	The polypeptides are used to identify compounds which bind to the	
CC	CC	polypeptides. Polynucleotides of the invention are used as probes and	
CC	CC	primers, for sequencing, for chromosome or gene mapping, in the	
CC	CC	production of recombinant proteins, and in generating anti-sense DNA or	
CC	CC	RNA and in gene therapy. Polypeptides of the invention can be used to	
CC	CC	target drugs to a tumour, in assays to determine biological activity, to	
CC	CC	raise antibodies/elicit an immune response, to determine quantitative	
CC	CC	protein levels, as tissue markers and to isolate receptors or ligands.	

Search completed: September 23, 2002, 17:59:00  
Job time: 7024 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:47:27 ; Search time 6364.12 Seconds  
(without alignments)  
1397.199 Million cell updates/sec

Title: US-09-019-441-4

Perfect score: 411

Sequence: 1 ATGAGATTGGGTGACGTG.....TCTGTGTCACGTCCTCTCA 411

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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33: /cgn2_6/ptodata/1/pna/US098C_COMB.seq.*
34: /cgn2_6/ptodata/1/pna/US099A_COMB.seq.*
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36: /cgn2_6/ptodata/1/pna/US099C_COMB.seq.*
37: /cgn2_6/ptodata/1/pna/US100_COMB.seq.*
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47: /cgn2_6/ptodata/1/pna/US6008_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	411	100.0	411	14	US-09-019-441-4
2	407.8	99.2	411	16	US-09-292-053-7
3	358.4	87.2	19040	17	US-09-343-485A-3
4	282.6	68.8	1710	23	US-09-617-746A-100
5	282.6	68.8	1710	24	US-09-631-451A-100
6	282.6	68.8	1721	23	US-09-617-746A-97
7	282.6	68.8	1721	24	US-09-631-451A-97
8	276.8	67.3	1709	17	US-09-359-922-264
9	276.8	67.3	1709	17	US-09-359-922-264
10	274	66.7	591	25	US-09-652-127-9891
11	274	66.7	591	27	US-09-698-010-15656
12	274	66.7	591	28	US-09-710-281-5766
13	267.4	65.1	411	16	US-09-269-332-58
14	267.4	65.1	411	18	US-09-423-800-58
15	267.4	65.1	411	37	US-10-019-501-58
16	267.4	65.1	411	37	US-10-019-571-58
17	267.4	65.1	411	37	US-10-019-785-58
18	266	64.7	1458	23	US-09-617-746A-193
19	266	64.7	1458	24	US-09-631-451A-193
20	265.8	64.7	3041	25	US-09-652-125A-9393
21	265.8	64.7	3041	25	US-09-652-127-9452
22	265.8	64.7	3041	25	US-09-652-916-10122
23	265.8	64.7	3041	27	US-09-699-999-7481
24	265.8	64.7	3041	28	US-09-710-281-5795
25	265.8	64.7	3041	28	US-09-716-475-7305
26	265.8	64.7	3041	29	US-09-726-175-3019
27	265.8	64.7	3041	29	US-09-726-176-1849
28	265.8	64.7	3041	29	US-09-726-211-1347
29	265.2	64.5	645	1	PCT-US01-08655-72
30	265.2	64.5	690	26	US-09-668-317-73
31	265.2	64.5	690	38	US-10-105-891-73
					Sequence 4, Appli
					Sequence 7, Appli
					Sequence 3, Appli
					Sequence 100, App
					Sequence 100, App
					Sequence 97, Appl
					Sequence 97, Appl
					Sequence 264, App
					Sequence 264, App
					Sequence 9891, Ap
					Sequence 15656, A
					Sequence 5766, Ap
					Sequence 58, Appl
					Sequence 58, Appl
					Sequence 58, Appl
					Sequence 58, Appl
					Sequence 193, App
					Sequence 193, App
					Sequence 9393, Ap
					Sequence 9452, Ap
					Sequence 10122, A
					Sequence 7481, Ap
					Sequence 5795, Ap
					Sequence 7305, Ap
					Sequence 3019, Ap
					Sequence 1849, Ap
					Sequence 1347, Ap
					Sequence 72, Appl
					Sequence 73, Appl

32	263.6	64.1	432	18	US-09-431-517-21418
33	262.2	63.8	1983	18	US-09-491-404-2415
34	262.2	63.8	1983	34	US-09-922-279-2415
35	262.2	63.8	1983	34	US-09-922-279A-2415
36	262	63.7	520	32	US-09-844-684-10
37	261.6	63.6	413	16	US-09-293-973-4372
38	261.6	63.6	413	34	US-09-904-939-4372
39	261.6	63.6	1741	23	US-09-617-746A-98
40	261.6	63.6	1741	24	US-09-631-451A-98
41	261.2	63.6	414	8	US-08-471-986-9
42	261.2	63.6	1366	18	US-09-491-404-3094
43	261.2	63.6	1366	34	US-09-922-279-3094
44	261.2	63.6	1366	34	US-09-922-279A-3094
45	261	63.5	630	32	US-09-844-684-14

## ALIGNMENTS

RESULT 1  
US-09-019-441-4  
; Sequence 4, Application US/09019441  
; GENERAL INFORMATION:  
; APPLICANT: REFF, Mitchell E.  
; KLOETZER, William S.  
; NAKAMURA, Takehiko  
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
; ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP  
; STREET: P. O. Box 1404

Query Match 100.0%; Score 411; DB 14; Length 411;

Best Local Similarity 100.0%; Pred. No. 2e-103; .		Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGAGTTTGGGCTCAGCTGGGTTTTCCTCTGTTTCAAGGTGTCCAGTGTGAG	60
Db	1 ATGGAGTTTGGGCTCAGCTGGGTTTTCCTCTGTTTCAAGGTGTCCAGTGTGAG	60
QY	61 GTGCAGCTGTGGAGTCTGTGGGGGGCTTGCAAGCCTGGGGGTCCCTCAGACTCTGG	120
Db	61 GTGCAGCTGTGGAGTCTGTGGGGGGCTTGCAAGCCTGGGGGTCCCTCAGACTCTGG	120
QY	121 TGGCAGGCTCCGGTTTCAGGTTTCACTTCAATAACTACTATCGAGTGGGTCCGCCAG	180
Db	121 TGGCAGGCTCCGGTTTTCAGGTTTCACTTCAATAACTACTATCGAGTGGGTCCGCCAG	180
QY	181 GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGTGTATCCACATGG	240
Db	181 GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGTGTATCCACATGG	240
QY	241 TACGCAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGACGCCAACACACACTG	300
Db	241 TACGCAGACTCCGTGAAGGGCAGATTACCATCTCCAGAGAGACGCCAACACACACTG	300
QY	301 TTTCTTCAAAATGAACAGCCTCAGAGCTCAGACACGGCTGTCTATTACTGTGCAGCTTG	360
Db	301 TTTCTTCAAAATGAACAGCCTCAGAGCTCAGACACGGCTGTCTATTACTGTGCAGCTTG	360
QY	361 ACTACAGGGTCTGACTCTGTGGGGCAGGGAGTCTGTGTACCGTCTCCTCA	411
Db	361 ACTACAGGGTCTGACTCTGTGGGGCAGGGAGTCTGTGTACCGTCTCCTCA	411

## RESULT 2

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US-09-292-053-7
; Sequence 7, Application US/09292053
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL E.
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: NAKAMURA, TAKEHIKO
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
; TITLE OF INVENTION: THEREOF AS THERAPEUTICS
; FILE REFERENCE: 23522.0699
; CURRENT APPLICATION NUMBER: US/09/292,053
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 08/803,085
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(58)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
; NAME/KEY: CDS
; LOCATION: (1)..(411)
US-09-292-053-7

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Query Match 99.2%; Score 407.8; DB 16; Length 411;  
Best Local Similarity 99.5%; Pred. NO. 1.6e-102;  
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;





Db 516 ttcccgatatttgactactggggccagggaaccctggtccacgcttc 562

## RESULT 5

US-09-631-451A-100

; Sequence 100, Application US/09631451A

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Zhou, Ping

; APPLICANT: Qian, Xiaohong B.

; APPLICANT: Wang, Zhiwei

; APPLICANT: Chen, Rui-hong

; APPLICANT: Asundi, Vinod

; APPLICANT: Cao, Yicheng

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: Novel Nucleic Acids and

; FILE REFERENCE: 785CIP2B

; CURRENT APPLICATION NUMBER: US/09/631,451A

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 09/617,746

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-25

; NUMBER OF SEQ ID NOS: 220

; SOFTWARE: pt\_FL\_genes Version 1.0

; SEQ ID NO 100

; LENGTH: 1710

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (162)..(1253)

US-09-631-451A-100

Query Match 68.8%; Score 282.6; DB 24; Length 1710;

Best Local Similarity 82.8%; Pred. No. 1.3e-67;

Matches 337; Conservative 0; Mismatches 64; Indels 6; Gaps 1;

QY 1 ATCGAGCTTTGGCGTGAAGGCGGCTTTCCCTGTCTCTCTTTTGAAGGCTGCCAGTGTGAG 60

Db 162 atggagtttgggctgagctggcttttctgtgctattttaaagggtgccagtgtag 221

QY 61 GTGACGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTGG 120

Db 222 gtgcagctgtgagctgtgggagggcttggtagagccttggggtccctggagactctcc 281

QY 121 TCGCAGCCTCCGGGTTCAGGTTCACTTCAATACTACTACATGAGCTGGGTCCGCCAG 180

Db 282 tgtgcagcctctg-----gattcaccttttagcagtttttcgatgagctgggtccgcca 335

QY 181 GCTCCAGGCGAGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGTATCCACATCG 240

Db 336 gtccagggaaggctggagtggttctcatctatttagtggtagtccgggtaccacatc 395

QY 241 TACGACAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAAAGCCCAACACACACTG 300

Db 396 tacgcagactcctgtaaggccggttccacctccacagagacaattcccaagaacgcgtg 455

QY 301 TTCTTCAATGAACAGCCTGAGAGTGGAGACAGCGCTGTCTATTACTGTCCGAGCTTG 360

Db 456 tatctgcaaatgaacagcctgagagccgaggaacgcgtatattactgtgcaaacccg 515

QY 361 ACTACAGGCTCTGACTCTCTGGGGCCAGGAGTCCCTGGTCCACCGTCTC 407

Db 516 ttcccgatatttgactactggggccagggaaccctggtccacgcttc 562

## RESULT 6

US-09-617-746A-97

; Sequence 97, Application US/09617746A

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Zhou, Ping

; APPLICANT: Qian, Xiaohong B.

; APPLICANT: Wang, Zhiwei

; APPLICANT: Chen, Rui-hong

; APPLICANT: Asundi, Vinod

; APPLICANT: Cao, Yicheng

; APPLICANT: Tillinghast, John

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: Novel Nucleic Acids and

; FILE REFERENCE: 21272-017CIP2A (785CIP2A)

; CURRENT APPLICATION NUMBER: US/09/617,746A

; CURRENT FILING DATE: 2000-07-01

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-25

; NUMBER OF SEQ ID NOS: 220

; SOFTWARE: pt\_FL\_genes Version 1.0

; SEQ ID NO 97

; LENGTH: 1721

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (162)..(1085)

US-09-617-746A-97

Query Match 68.8%; Score 282.6; DB 23; Length 1721;

Best Local Similarity 82.8%; Pred. No. 1.3e-67;

Matches 337; Conservative 0; Mismatches 64; Indels 6; Gaps 1;

QY 1 ATCGAGCTTTGGCGTGAAGGCGGCTTTCCCTGTCTCTCTTTTGAAGGCTGCCAGTGTGAG 60

Db 162 atggagtttgggctgagctggcttttctgtgctattttaaagggtgccagtgtag 221

QY 61 GTGACGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTGG 120

Db 222 gtgcagctgtgagctgtgggagggcttggtagagccttggggtccctggagactctcc 281

QY 121 TCGCAGCCTCCGGGTTCAGGTTCACTTCAATACTACTACATGAGCTGGGTCCGCCAG 180

Db 282 tgtgcagcctctg-----gattcaccttttagcagtttttcgatgagctgggtccgcca 335

QY 181 GCTCCAGGCGAGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGTATCCACATCG 240

Db 336 gtccagggaaggctggagtggttctcatctatttagtggtagtccgggtaccacatc 395

QY 241 TACGACAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAAAGCCCAACACACACTG 300

Db 396 tacgcagactcctgtaaggccggttccacctccacagagacaattcccaagaacgcgtg 455

QY 301 TTCTTCAATGAACAGCCTGAGAGTGGAGACAGCGCTGTCTATTACTGTCCGAGCTTG 360

Db 456 tatctgcaaatgaacagcctgagagccgaggaacgcgtatattactgtgcaaacccg 515

QY 361 ACTACAGGCTCTGACTCTCTGGGGCCAGGAGTCCCTGGTCCACCGTCTC 407

Db 516 ttcccgatatttgactactggggccagggaaccctggtccacgcttc 562

## RESULT 7

US-09-631-451A-97

; Sequence 97, Application US/09631451A

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Zhou, Ping

; APPLICANT: Qian, Xiaohong B.

; APPLICANT: Wang, Zhiwei

; APPLICANT: Chen, Rui-hong  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Cao, Yicheng  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 785CIP2B  
; CURRENT APPLICATION NUMBER: US/09/631,451A  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 97  
; LENGTH: 1721  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (162)..(1085)  
US-09-631-451A-97

Query Match 68.8%; Score 282.6; DB 24; Length 1721;  
Best Local Similarity 82.8%; Pred. No. 1.3e-67;  
Matches 337; Conservative 0; Mismatches 64; Indels 6; Gaps 1;  
QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTTTTCCCTTTTGAAGAGTGTCCAGTGTGAG 60  
Db 162 atggagttgggctgagctgggttttcccttttgaagagtgtccagtgtgag 221  
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120  
Db 222 gtgcagctgttgagctgggtgggagctgtgacagcctgggggtccctgagactctcc 281  
QY 121 TGGCAGCTCCGGGTTACAGTTCACCTTCAATTAAGTGTGAGTGTGAGTGTGAGTGTGAG 180  
Db 282 tggcagctccgggttacagttcaccttcaatgaagtgtgagtgtagtgagtgagtgagtgag 335  
QY 181 GTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGTGATGCCACATGG 240  
Db 336 gtccagggaaggctggagtggtctcatctattagtgtagtgagtgagtgagtgagtgagtgag 395  
QY 241 TAGCGAGACTCCGTGAAGGGCAGATTTCACCATCTCCAGAGAGAACGCCAACACACACTG 300  
Db 396 tagcgagactccgtgaaggccaggttcacatctccagagagacaattcccaagaacacgctg 455  
QY 301 TTCTTCAATGAACAGCCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360  
Db 456 tatctgcaatgaacagcctgagagtcgagagcagcggttatattactgtgcgaacacg 515  
QY 361 ACTACAGGCTGTGACTTCCCTGGGGCCAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 407  
Db 516 ttctcgattttgactactggggccagggaggaacccctggtcacccgtctc 562

RESULT 8  
US-09-922-264/c  
; Sequence 264, Application US/09359922  
; GENERAL INFORMATION:  
; APPLICANT: Hysq, Inc.  
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA  
; TITLE OF INVENTION: LIBRARIES  
; FILE REFERENCE: 20411-752CON1  
; CURRENT APPLICATION NUMBER: US/09/359,922  
; CURRENT FILING DATE: 1999-07-22  
; EARLIER APPLICATION NUMBER: US 09/205,155  
; EARLIER FILING DATE: 1998-12-03  
; NUMBER OF SEQ ID NOS: 13203  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 264

; LENGTH: 1709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-359-922-264

Query Match 67.3%; Score 276.8; DB 17; Length 1709;  
Best Local Similarity 82.1%; Pred. No. 5.3e-66;  
Matches 353; Conservative 0; Mismatches 52; Indels 25; Gaps 2;  
QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTTTTCCCTTTTGAAGAGTGTCCAGTGTGAG 60  
Db 1546 atggagttgggctgagctgggttttcccttttcccttttgaagagtgtccagtgtgag 1487  
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCCTGAGACTCTGG 120  
Db 1486 gtgcagctggtggagctggggcggttggcaagccctgggggtccctgagactctcc 1427  
QY 121 TGGCAGCTCCGGGTTACAGTTCACCTTCAATTAAGTGTGAGTGTGAGTGTGAGTGTGAG 180  
Db 1426 tggcagctccgggttacagttcaccttcaatgaagtgtgagtgtagtgagtgagtgagtgag 1373  
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGTGATGCCACATGG 240  
Db 1372 gctccaggcgaaggctggagtggtctcatatattagtagtagtgagtgagtgagtgagtgag 1313  
QY 241 TAGCGAGACTCCGTGAAGGGCAGATTTCACCATCTCCAGAGAGAACGCCAACACACACTG 300  
Db 1312 tagcgagactccgtgaaggccagatttcacatctccagagagacaacgccaaagaaactcactg 1253  
QY 301 TTCTTCAATGAACAGCCTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 360  
Db 1252 ttcttcaatgaacagcctgagagtgtagtgagtgagtgagtgagtgagtgagtgagtgagtgag 1193  
QY 361 ACTACAGG-----TCTGACTCTCTGGGGCCAGGAGTGTGAGTGTGAGTGTGAGTGTGAG 401  
Db 1192 ccctcagcgtctgtctgctcccttccacatgactcttggggccaggaaacctgtgtcac 1133  
QY 402 CGTCTCCTCA 411  
Db 1132 cgtctcctca 1123

RESULT 9  
US-09-359-922-264/c  
; Sequence 264, Application US/09359922A  
; GENERAL INFORMATION:  
; APPLICANT: Leshkowitz, Dena  
; APPLICANT: Liu, Jin  
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA  
; TITLE OF INVENTION: LIBRARIES  
; FILE REFERENCE: 20411-752CON1  
; CURRENT APPLICATION NUMBER: US/09/359,922A  
; CURRENT FILING DATE: 1999-07-22  
; EARLIER APPLICATION NUMBER: US 09/205,155  
; EARLIER FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: US 09/034,341  
; EARLIER FILING DATE: 1998-02-13  
; NUMBER OF SEQ ID NOS: 13203  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 264  
; LENGTH: 1709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-359-922-264

Query Match 67.3%; Score 276.8; DB 17; Length 1709;  
Best Local Similarity 82.1%; Pred. No. 5.3e-66;  
Matches 353; Conservative 0; Mismatches 52; Indels 25; Gaps 2;  
QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTTTTCCCTTTTGAAGAGTGTCCAGTGTGAG 60  
Db 1546 atggagttgggctgagctgggttttcccttttcccttttgaagagtgtccagtgtgag 1487

Db	1546	ATGCAGTTTCGGCTGAGCTGGGTTTTTCCTTTGTTGCTATTTTAGAAGGTGTCCACTGTGAG	1487
Qy	61	GTGCAGCTGTGTGAGTCTGGGGCGGCTTTGGCAAGCCTTGGGGGTCCCTCAGACTCTGG	120
Db	1486	GTGCAGCTGTGTGAGTCTGGGGGAGCTTGGTCCAGCCTGGGGGTCCCTCAGACTCTCC	1427
Qy	121	TGGCAGCCTCCGGTTTCAGGTTTCACTTCAATACTACTATCAGGACTGGGTCCGCCAG	180
Db	1426	TGTGCAGCCTCTG-----GATTCACTTCAATGATTATGCATCAGCTGGGTCCGCCAG	1373
Qy	181	GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTACTAGTGTGATCCACATGG	240
Db	1372	GCTCCAGGCNAGGGCTGGAGTGGGTCTCATACATTAGTAGGGGTGTGAGCATAC	1313
Qy	241	TACGCAGACTCCGTGAAGGCGGATTCACATCTCCAGAGAGACGGCAACAACACACTG	300
Db	1312	TACGCAGACTCTGTGAAGGCGGATTCACATCTCCAGAGACAAGCCAGAACTCACTG	1253
Qy	301	TTTCTTCAATGAACGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGTTG	360
Db	1252	TATCTGCAATGAACGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGA	1193
Qy	361	ACTACAGG-----TCTGACTCTCTGGGGCCAGGAGCTCTTGTCAC	401
Db	1192	CCCTCAGGGCTGCTGTGCTCTCCCTTCCACATGACTCTCTGGGGCCAGGGAACCTTGTCAC	1133
Qy	402	CGTCTCCTCA	411
Db	1132	CGTCTCCTCA	1123

```

RESULT 10
US-09-652-127-9891
; Sequence 9891, Application us/09652127
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1183-001
; CURRENT APPLICATION NUMBER: US/09/652,127
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,134
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 10475
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9891
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-127-9891

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Query Match	66.7%	Score 274;	DB 25;	Length 591;
Best Local Similarity	82.1%	Pred. No. 2.4e-65;		
Matches 345; Conservative	0;	Mismatches 60;	Indels 15;	Gaps 2;
QY	1	ATGGAGTTTGGCGTGA	CTGGGTTTCTCTTCTCTTTGAAGG	GTCCAGTGTGAG 60
Db	96	atggaactgggggtccgc	gtgtttccctgtgtctatttagaagg	tggtccagtgtag 155
QY	61	GTGCAGCTGGTGGAG	CTGTGGGGGGCGGTGGCAAGCGTGGGGGT	CCCTGAGACTCTGG 120
Db	156	gtgcagctgtgtgagtc	gtgggaggttggtagcagcctggaggg	gtcctgagactctcc 215
QY	121	TGCGCAGCTCCGGGT	TCAGGTTCACTTCAACTAACTAACTACT	ATCATGTGACTGGTCCGCCAG 180
Db	216	tgtgtagccctcg----	gattcaacctttagtagttatgaaatgaa	ttgggtccgccaag 269
QY	181	GTCTCCAGGGCAGGG	CTGGGCTGGAGTGGGTCTCAGTATTAGT	AGTGGTGATCCCAATGG 240
Db	270	gctccagggaaagggtc	gtgagtggttttcacatttagtagtagt	gtgtagaacatttc 329
QY	241	TAGCGACACTCCGT	TGAAGGGCAGATTCAACCATCTCCAG	AGAGAACGCCCAACCAACTGT 300

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Db      330  tacgcagactctgtgaaggccgattccaccatctccagacacgccaagaactcactg      389
Qy      301  TTTTCTCAAAATGAACAGCCTGAGAGCTGAGGACACGCGTGTCTATTACTGTGGGAGCTTG      360
Db      390  tatctgcaaatgaacagccttgagagccgagagacacggtcttttattactgtcgagactc      449
Qy      361  ACTACAGG-----TCTGACTCTCTGGGGCCAGGAGTCTCTGTACCCGTCCTCTCA      411
Db      450  aatagtggagctactctttttgactactgggcccagggaaccctggtccacgctctcctca      509

RESULT 11
US-09-698-010-15656
; Sequence 15656: Application US/09698010
; GENERAL INFORMATION:
;   APPLICANT: Williamson, Mark
;   TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
;   TITLE OF INVENTION: THEREFOR
;   FILE REFERENCE: 1600.2029-001
;   CURRENT APPLICATION NUMBER: US/09/698,010
;   CURRENT FILING DATE: 2000-10-27
;   PRIOR APPLICATION NUMBER: 60/162,358
;   PRIOR FILING DATE: 1999-10-29
;   NUMBER OF SEQ ID NOS: 15684
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15656
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-698-010-15656

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Query Match	66.7%	Score 274;	DB 27;	Length 591;
Best Local Similarity	82.1%;	Pred. No. 2.4e-65;		
Matches 345;	Conservative 0;	Mismatches 60;	Indels 15;	Gaps 2
Qy 1	ATGAGATTGGGCTGAGCTGGGTTTCCCTGTCTCCTTTTCAAAGGTGTCAGTGTGAG 60			
Db 96	atggaactggggccgcgctgggtttctctgttctattttagaagggtgccagtgtag 155			
Qy 61	GTGAGCTGTGTGAGTCTGGGGGGCGGTTGGCAAAGCTGGGGGTCCCTGAGACTCTGG 120			
Db 156	gtcagctgtgtgagctctgggggaggtttgtacagcctggaagggtccctgagactctcc 215			
Qy 121	TGCGAGCCCTCCGGGTTCAGGTTCACTTCAATAACTACTACATGGACTGGGTCCGCCAG 180			
Db 216	tgtgtagccctcg-----gattcacctttagtagttatgaaatgaattgggtccgccag 269			

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Db      270  gctccagggaaggggctcgagtggtttccatacatagtagtagtgtagaaccatattc 329
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QY      241  TAGCCACAGCTCCGTGAAGGCGCAGATTCCACCATCTCCAGAGAGAACGCCAACACACACTG 300
      |||||
Db      330  tacgcagactctgtgaagggccgattccaccatctccagagacaacgcccaagaactcactg 389
      |||||
QY      301  TTCTCTCAAAATGAACGCCCTGACAGCTGAGGACACGCGCTCTCTATTACTCTCGGAGCTTG 360
      |||||
Db      390  tactctgaatgaacagcctgagagccgaggaacgcgtgtttattactgtgcgagactc 449
      |||||
QY      361  ACTACAGGG-----TCTGACTCTCTGGGGCCAGGGAGTCTGTGCTACCGTCTCCTCA 411
      |||||
Db      450  aatgatggagctactctttttgactactggggccagggaacctggctaccgtctctctca 509
      |||||

RESULT 12
US-09-710-281-5766
; Sequence 5766, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.

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US-09-423-800-58

Query Match	65.1%	Score 267.4	DB 18	Length 411
Best Local Similarity	81.3%	Pred. No. 1.5e-63		
Matches 339	Conservative	0	Mismatches 66	Indels 12
Gaps	2			
QY	1	ATGCAGTTGGGCTGAGCTGGGTTTCTCTGCTTCTCTTTTGAAGGTGTCAGCTGTCAG	60	
Db	1			
QY	1	atg999gttt999ct9agct999gtttctct9gtctcttttaa9ag9gtccag9gtcag	60	
Db	1			
QY	61	GTGCAGCTGTGTGAGTCTGGGGCGCGTGTGCAAAGCCTGGGGGGTCCCTGAGACTCTGG	120	
Db	61	gtgcagctgtgtgagctctg999gag9c9gtggtccagcctg99ag9tccc9gagactccc	120	
QY	121	TGCGCAGCCTCCGGTTCAGGTTCACTTCACTTCAATTAACACTACATGGACTGGTCCGCCAG	180	
Db	121	tgtcagccctctg-----gattcaccttcagtagctatggcattgttt99gtgcgcag	174	
QY	181	GCCTCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTAGTGGTGTATCCACATGG	240	
Db	175	gctccaggcaagg9cctg9agtg99gtg9caaccattagtagtg9gtagttacacctac	234	
QY	241	TACGCACACTCCGTGAGGGCAGATTCACTATCTCCAGAGAGACGCCACACACACTG	300	
Db	235	tatccagacag9t9aa999gc9attcaccatctccagagacaaattcccaagaac9cgtg	294	
QY	301	TTTCTTCAATATGACACGCTTGAGAGCTGAGACACGGCTGTCTATTATGTGCCAGTTG	360	
Db	295	tatctgcaaatgaacac9cct9agagct9ag9acac9c9ctgtgtattactgt9ag9acag	354	
QY	361	ACTACAGGCTGTGAC-----TCTTGGGGCAGGGACTCTGTGTCACCGTCTCTCA	411	
Db	355	actactatgacttactt9cttactgt99c9cag9gaac9cctgg9ccac9c9tctctca	411	

Search completed: September 23, 2002, 19:47:39  
Job time: 7034 sec

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RESULT 15
US-10-019-501-58
; Sequence 58, Application US/10019501
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: Ameliorative agent for low vasopressin concentration
; FILE REFERENCE: PH-944-PCT
; CURRENT APPLICATION NUMBER: US/10/019,501
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: JP 11-189322
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(411)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
US-10-019-501-58

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Query Match	65.1%	Score 267.4	DB 37	Length 411
Best Local Similarity	81.3%	Pred. No. 1.5e-63		
Matches 339	Conservative 0	Mismatches 66	Indels 12	Gaps 2
QY	1	ATGGAGCTTTGGCGTGAGCTGGGTTTCCCTTGTTCCTTTTGAAGAGGTGCCAGTCTGAG	60	
Db	1	atggggtttgggtgagctgggttttccctgtgtcttttaagagggtgccagtgctcag	60	
QY	61	GTGCAGCTGGTGGAGTCTGGGGCGCGCTTGGCGAAAAGCCTGGGGGGTCCCTGAGACATCTGG	120	
Db	61	gtgcagctggtagagtcctggggagagcgctgtgtccagacctgggaggtccctggaactctcc	120	

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 19:58:52 ; Search time 662.78 Seconds  
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1998.488 Million cell updates/sec

Title: US-09-019-441-4  
Perfect score: 411  
Sequence: 1 ATGAGTTTGGGTGACCTG.....TCTGTGTCACGCTCTCTCA 411

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2148580 seqs, 1611384217 residues

Total number of hits satisfying chosen parameters: 4297160

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
7: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq.\*  
8: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	411	100.0	411	7	US-10-103-686-4
2	276.8	67.3	1709	5	US-09-919-002-264
3	267.4	65.1	411	6	US-10-182-018-58
4	267.4	65.1	411	6	US-10-220-149-58
5	267.4	65.1	411	7	US-10-169-003-58
6	265.2	64.5	690	7	US-10-125-237-73
7	263.4	64.1	1426	1	PCT-US02-20181-1
8	262	63.7	520	7	US-10-040-244-10
9	261	63.5	630	7	US-10-040-244-14
10	257.8	62.7	580	7	US-10-040-244-12
11	256.4	62.4	1712	6	US-10-206-008-189
12	254.6	61.9	1392	7	US-10-153-382-1
13	254.6	61.9	1392	7	US-10-153-382-4
14	254.6	61.9	1999	7	US-10-153-382-2
15	253.2	61.6	1395	7	US-10-153-382-8
16	252.6	61.5	1392	7	US-10-153-382-12
17	250.8	61.0	1605	5	US-09-629-469A-18517
18	247.6	60.2	626	5	US-09-634-754C-28
19	247.6	60.2	626	5	US-09-634-754D-28
20	247.2	60.1	407	5	US-09-918-995-16657
21	244.4	59.5	1413	7	US-10-153-382-16
22	241.8	58.8	397	7	US-10-146-502-2106
23	241.2	58.4	1792	7	US-10-158-646-54
24	240	58.4	720	5	US-09-511-939-1
25	240	58.4	720	5	US-09-968-561A-1

ALIGNMENTS

RESULT 1  
US-10-103-686-4  
Sequence 4, Application US/10103686  
GENERAL INFORMATION:  
APPLICANT: REFF, Mitchell E.  
KLOETZER, William S.  
NAKAMURA, Takehiko  
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: P.O. Box 1404  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10103,686  
FILING DATE: 25-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/803,085  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Teskin, Robin L.  
REGISTRATION NUMBER: 35,030  
REFERENCE/DOCKET NUMBER: 012712-353  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 411 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..411  
FEATURE:  
NAME/KEY: mat\_peptide

26	239.6	58.3	496	6	US-10-206-008-401	Sequence 401, App
27	239.6	58.3	496	6	US-10-211-364-212	Sequence 212, App
28	239.6	58.3	1673	1	PCT-US02-18947-1932	Sequence 1932, Ap
29	239.6	58.3	1673	7	US-10-172-118-1932	Sequence 1932, Ap
30	238.4	58.0	348	1	PCT-US02-20332-75	Sequence 75, Appl
31	238	57.9	1664	6	US-10-206-008-198	Sequence 198, App
32	236.8	57.6	348	1	PCT-US02-20332-79	Sequence 79, Appl
33	235.4	57.3	457	6	US-10-206-008-411	Sequence 411, App
34	235.4	57.3	457	6	US-10-211-364-122	Sequence 122, App
35	235.4	57.3	457	6	US-10-222-860-318	Sequence 318, App
36	235.2	57.2	348	1	PCT-US02-20332-82	Sequence 82, Appl
37	234.4	57.0	400	5	US-09-918-995-16290	Sequence 16290, A
38	231.6	56.4	1640	6	US-10-206-008-187	Sequence 187, App
39	230.4	56.1	311	6	US-10-203-136-21308	Sequence 21308, A
40	230.4	56.1	311	6	US-10-203-135-20914	Sequence 20914, A
41	229.4	55.8	351	1	PCT-US02-00060A-25	Sequence 25, Appl
42	229.2	55.8	1404	1	PCT-US02-11853-18	Sequence 18, Appl
43	229.2	55.8	3244	1	PCT-US02-11853-16	Sequence 16, Appl
44	228.4	55.6	4026	5	US-09-949-039-1	Sequence 1, Appl
45	226	55.0	413	5	US-09-918-995-16675	Sequence 16675, A

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; LOCATION: 58..411
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-103-686-4

Query Match 100.0%; Score 411; DB 7; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.7e-95;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 ATGCAGTTTGGGCTGACCTGGGTTTTCCCTGTGTCCTTTTGAAGAGTGTCCAGTGTGAG 60
DB 1 ATGCAGTTTGGGCTGACCTGGGTTTTCCCTGTGTCCTTTTGAAGAGTGTCCAGTGTGAG 60
QY 61 GTGCAGCTGTTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGTGCCCTGAGACTCTGG 120
DB 61 GTGCAGCTGTTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGTGCCCTGAGACTCTGG 120
QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAACTACTACATGAGCTGGGTCCGCCAG 180
DB 121 TGGCAGCCTCCGGGTTTCAGGTTTCACTTCAATAACTACTACATGAGCTGGGTCCGCCAG 180
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGCATCCACATGG 240
DB 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGCATCCACATGG 240
QY 241 TACGCAGACTCCGTGAAGGCGACATTCACCATCTCCAGAGAGAAGCCAAACACACTG 300
DB 241 TACGCAGACTCCGTGAAGGCGACATTCACCATCTCCAGAGAGAAGCCAAACACACTG 300
QY 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
DB 301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
QY 361 ACTACAGGGTCTCACTCTGGGGCCAGGAGTCTGGTCAACGCTCTCTCTCA 411
DB 361 ACTACAGGGTCTCACTCTGGGGCCAGGAGTCTGGTCAACGCTCTCTCTCA 411

RESULT 2
US-09-919-002-264/c
; Sequence 264, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-264

Query Match 67.3%; Score 276.8; DB 5; Length 1709;
Best Local Similarity 82.1%; Pred. No. 7.6e-61;
Matches 353; Conservative 0; Mismatches 52; Indels 25; Gaps

QY 1 ATGCAGTTTGGGCTGAGCTGGGTTTTCCCTGTGTCCTTTTGAAGAGTGTCCAGTGTGAG 60
DB 1546 ATGCAGTTTGGGCTGAGCTGGGTTTTCCCTGTGTCCTATTAGAGAGTGTCCAGTGTGAG 1487
QY 61 GTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGTGCCCTGAGACTCTGG 120
DB 1486 GTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGTGCCCTGAGACTCTGG 1427

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Db 235 tatccagacagtgtgaagggcgattaccatctccagagacaattcccaagaacacgctg 294  
QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGCTTATTACTGTGCGAGCTTG 360  
Db 295 tatctgaaatgaacagcctgagctgagacacggctgtgtattactgtgcgagacag 354  
QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCAGGAGTCTGTGTCACCGTCTCCTCA 411  
Db 355 actactagacttacttcttactgtggccagggaacccctgtccaccgtctctctca 411

## RESULT 4

US-10-220-149-58

; Sequence 58, Application US/10220149

; GENERAL INFORMATION:

; APPLICANT: CHUGAI PHARMACEUTICAL CO., LTD.

; TITLE OF INVENTION: Tissue degradation inhibiting agent

; FILE REFERENCE: PH-1015-PCT

; CURRENT APPLICATION NUMBER: US/10/220,149

; PRIOR FILING DATE: 2002-08-27

; PRIOR APPLICATION NUMBER: JP2000-52414

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 58

; LENGTH: 411

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(411)

; NAME/KEY: mat\_peptide

; LOCATION: (58)..(411)

; US-10-220-149-58

Query Match 65.1%; Score 267.4; DB 6; Length 411;  
Best Local Similarity 81.3%; Pred. No. 1.7e-58;  
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTTGTTCCCTTTTGAAGAGGTGCCAGTGTGAG 60  
Db 1 atggggtttggcgtgagctgggttttccctgtgctctttaaagaggtgtccagtgctag 60

QY 61 GTCAGCTGTGTGAGTCTGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120  
Db 61 gtgcagctgtgtgagctgtggggagcgctgtccagcctgggaggtccctgagactctcc 120

QY 121 TGGCAGCCTCCGGTTCAGGTTTCACCTTCAATAACTACTACATGGACTGGTCCGCCAG 180  
Db 121 tgtgcagcctctg-----gattcaccctcagtagctatggcatgtcttgggtccgcag 174

QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTACGTTATTAGTAGTAGTGTGATCCACATGG 240  
Db 175 gctccaggcaaggcgtgagtgagggtggcaaccattagtagtggtgtagttacacctac 234

QY 241 TAGCAGACTCTCCGTGAAGGCGCATTCACCATCTCCAGAGAACGCCAACACACTG 300  
Db 235 tatccagacagtgtgaaggggcgattccaccatctccagagacaattcccaagaacacgctg 294

QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGCTTATTACTGTGCGAGCTTG 360  
Db 295 tatctgcaaatgaacagcctgagctgaggaacacgctgtgtattactgtgcgagacag 354

QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCAGGAGTCTGTGTCACCGTCTCCTCA 411  
Db 355 actactagacttacttcttactgtggccagggaacccctgtccaccgtctctctca 411

## RESULT 5

US-10-169-003-58

; Sequence 58, Application US/10169003

; GENERAL INFORMATION:  
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA  
; TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical Preparation  
; FILE REFERENCE: PH-1093-PCT  
; CURRENT APPLICATION NUMBER: US/10/169,003  
; CURRENT FILING DATE: 2002-06-26  
; PRIOR APPLICATION NUMBER: JP 11-375203  
; PRIOR FILING DATE: 1999-12-28  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 411  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(411)  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: (58)..(411)  
; US-10-169-003-58

Query Match 65.1%; Score 267.4; DB 7; Length 411;  
Best Local Similarity 81.3%; Pred. No. 1.7e-58;  
Matches 339; Conservative 0; Mismatches 66; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGCTGAGCTGGGTTTCCTTTGTTCCCTTTTGAAGAGGTGCCAGTGTGAG 60  
Db 1 atggggtttggcgtgagctgggttttccctgtgctctttaaagaggtgtccagtgctag 60

QY 61 GTCAGCTGTGTGAGTCTGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120  
Db 61 gtgcagctgtgtgagctgtggggagcgctgtccagcctgggaggtccctgagactctcc 120

QY 121 TGGCAGCCTCCGGTTCAGGTTTCACCTTCAATAACTACTACATGGACTGGTCCGCCAG 180  
Db 121 tgtgcagcctctg-----gattcaccctcagtagctatggcatgtcttgggtccgcag 174

QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTACGTTATTAGTAGTAGTGTGATCCACATGG 240  
Db 175 gctccaggcaaggcgtgagtgagggtggcaaccattagtagtggtgtagttacacctac 234

QY 241 TAGCAGACTCTCCGTGAAGGCGCATTCACCATCTCCAGAGAACGCCAACACACTG 300  
Db 235 tatccagacagtgtgaaggggcgattccaccatctccagagacaattcccaagaacacgctg 294

QY 301 TTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGCTTATTACTGTGCGAGCTTG 360  
Db 295 tatctgcaaatgaacagcctgagctgaggaacacgctgtgtattactgtgcgagacag 354

QY 361 ACTACAGGCTCTGAC-----TCCTGGGGCAGGAGTCTGTGTCACCGTCTCCTCA 411  
Db 355 actactagacttacttcttactgtggccagggaacccctgtccaccgtctctctca 411

## RESULT 6

US-10-125-237-73

; Sequence 73, Application US/10125237

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chinghua

; APPLICANT: Zhou, Ping

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Zhao, Qing A.

; APPLICANT: Xue, Aidong J.

; APPLICANT: Zhang, Jie

; APPLICANT: Wehrman, Tom

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: Novel Nucleic Acids and

; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 79ICIP2ADIV  
; CURRENT APPLICATION NUMBER: US/10/125,237  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: 09/668,317  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/552,929  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 73  
; LENGTH: 690  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (97)..(507)  
US-10-125-237-73

Query Match 64.5%; Score 265.2; DB 7; Length 690;  
Best Local Similarity 86.2%; Pred. No. 6.3e-58;  
Matches 307; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCTTGTCTCTCTTTTGAAGGTTCCAGTGTGAG 60  
Db 97 atggagttgggctgagctgggtttcccttgtctctcttttgaagggttccagtgtag 156  
QY 61 GTGCAGCTGGTGGAGCTCGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTGG 120  
Db 157 gtcgagctgggtggagctcgccggggaggttagttcagcctgggggtccctgagactctcc 216  
QY 121 TGGCAGCTCGGGTTTCAAGTTCACCTTCAATACTAGTACGACTGGGTCCGCCAG 180  
Db 217 tgtgcagctctg-----gattcaccttcagtagctactgagtgagtgccgcaa 270  
QY 181 GCTCCAGGCGAGGGTGGTGGTCTCAGCTATTAGTAGTGGTATCCCATGG 240  
Db 271 gctccaggaggggctggtggtgtcagctattatagtgaggtagcacaagc 330  
QY 241 TAGCAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAACGCCAACACACACTG 300  
Db 331 tacgggactcctgtaaggccgattcacctctccagagacaacgcgcaagcgtcg 390  
QY 301 TTCTTCAATGAACAGCTGAGAGCTGAGGCTGCTCTATTACTGTCTGCTGCGAG 356  
Db 391 tatctgcaaatgaacagctgtagagccgagagacagcgctgtgtattactgtgcaag 446

RESULT 7  
PCT-US02-20181-1  
; Sequence 1, Application PC/TUS0220181  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J  
; APPLICANT: Martin, Francis H  
; APPLICANT: Corvalan, Jose R  
; APPLICANT: Davis, C. Geoffrey  
; TITLE OF INVENTION: Antibodies to OPGL  
; FILE REFERENCE: 06843.0049-00000  
; CURRENT APPLICATION NUMBER: PCT/US02/20181  
; CURRENT FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: 60/301,172  
; PRIOR FILING DATE: 2001-06-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1426  
; TYPE: DNA  
; ORGANISM: Mus musculus  
PCT-US02-20181-1

Query Match 64.1%; Score 263.4; DB 1; Length 1426;

Best Local Similarity 80.2%; Pred. No. 1.9e-57;  
Matches 344; Conservative 0; Mismatches 61; Indels 24; Gaps 2;  
QY 1 ATGGAGTTGGGCTGAGCTGGGTTTTCCTTGTCTCTCTTTTGAAGGTTCCAGTGTGAG 60  
Db 14 atggagttgggctgagctgggttttcttctgtgctattttaaagggtgccagtgtag 73  
QY 61 GTGCAGCTGGTGGAGCTCGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTGG 120  
Db 74 gtcgagctgttgagctctgggggaggttggttacagcctggggggtccctgagactctcc 133  
QY 121 TGGCAGCTCGGGTTTCAAGTTCACCTTCAATACTAGTACGACTGGGTCCGCCAG 180  
Db 134 tgtgcagctctg-----gattcaccttcagtagctactgagctgggtccgccaag 187  
QY 181 GCTCCAGGCGAGGGTGGTGGTCTCAGCTATTAGTAGTGGTATCCCATGG 240  
Db 188 gctccaggaggggctggtggtgtcagctattactggtggtggtgtagtatac 247  
QY 241 TAGCAGACTCCGTGAAGGCGAGATTACCATCTCCAGAGAACGCCAACACACACTG 300  
Db 248 tacgagactcctgtaaggccggttcaccatctccagagacaattccaagaacacgctg 307  
QY 301 TTCTTCAATGAACAGCTGAGAGCTGAGGCTGCTCTATTACTGTCTGCTGCGGA----- 355  
Db 308 tatctgcaaatgaacagctgtagagccgagagacagcgccgtatattactgtgcgaaagat 367  
QY 356 -----GCTTGACTACAGGGTCTGACTCTCTGGGCGCAGGAGTCTCTGGTCACC 402  
Db 368 ccaggagactacggtgattatggttgcgacccctggggccaggaaacctggtccacc 427  
QY 403 GTCTCTCTCA 411  
Db 428 gctcctca 436

## RESULT 8

US-10-040-244-10  
; Sequence 10, Application US/10040244  
; GENERAL INFORMATION:  
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA  
; APPLICANT: FORCE, WALKER F  
; APPLICANT: TAKAHASHI, NOBUAKI  
; APPLICANT: MIKAYAMA, TOSHIFUMI  
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI  
; FILE REFERENCE: 021286/0272501  
; CURRENT APPLICATION NUMBER: US/10/040,244  
; CURRENT FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: 60/200,601  
; PRIOR FILING DATE: 2000-4-28  
; PRIOR APPLICATION NUMBER: PCT/US01/13672  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: 09/844,684  
; PRIOR FILING DATE: 2001-04-27  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 10  
; LENGTH: 520  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-244-10

Query Match 63.7%; Score 262; DB 7; Length 520;  
Best Local Similarity 85.7%; Pred. No. 4e-57;  
Matches 305; Conservative 0; Mismatches 45; Indels 6; Gaps 1;

QY 1 ATGGAGTTGGGCTGAGCTGGGTTTTCCTTGTCTCTTTTGAAGGTTCCAGTGTGAG 60  
Db 32 atggagttgggctgagctgggttttcttctgtgtatttttaaagggtgccagtgtag 91  
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTGAGACTCTGG 120  
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;; PRIOR APPLICATION NUMBER: 60/214,886  
;; PRIOR FILING DATE: 2000-06-28  
;; PRIOR APPLICATION NUMBER: 60/217,487  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,758  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/220,963  
;; PRIOR FILING DATE: 2000-07-26  
;; PRIOR APPLICATION NUMBER: 60/217,496  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,447  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/218,290  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/225,757  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/226,868  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/216,647  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,267  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/216,880  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,270  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/251,869  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/235,834  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: 60/234,274  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: 60/234,223  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: 60/228,924  
;; PRIOR FILING DATE: 2000-08-30  
;; PRIOR APPLICATION NUMBER: 60/224,518  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/236,369  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/224,519  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/220,964  
;; PRIOR FILING DATE: 2000-07-26  
;; PRIOR APPLICATION NUMBER: 60/241,809  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/249,299  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/236,327  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/241,785  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/244,617  
;; PRIOR FILING DATE: 2000-11-01  
;; PRIOR APPLICATION NUMBER: 60/225,268  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/236,368  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/251,856  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/251,868  
;; PRIOR FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/229,344  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/234,997  
;; PRIOR FILING DATE: 2000-09-25  
;; PRIOR APPLICATION NUMBER: 60/229,343  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,345  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,287  
;; PRIOR FILING DATE: 2000-09-01  
;; PRIOR APPLICATION NUMBER: 60/229,513  
;; PRIOR FILING DATE: 2000-09-05  
;; PRIOR APPLICATION NUMBER: 60/231,413  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/229,509  
;; PRIOR FILING DATE: 2000-09-05  
;; PRIOR APPLICATION NUMBER: 60/236,367  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/237,039  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,038  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/236,370  
;; PRIOR FILING DATE: 2000-09-29  
;; PRIOR APPLICATION NUMBER: 60/236,802  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,037  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/237,040  
;; PRIOR FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 60/240,960  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/239,935  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: 60/239,937  
;; PRIOR FILING DATE: 2000-10-13  
;; PRIOR APPLICATION NUMBER: 60/241,787  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,474  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/246,532  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/249,216  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,210  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/226,681  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/225,759  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/225,213  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/227,182  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/225,214  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/235,836  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: 60/230,438  
;; PRIOR FILING DATE: 2000-09-06  
;; PRIOR APPLICATION NUMBER: 60/215,135  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: 60/225,266  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/249,218  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,208  
;; PRIOR FILING DATE: 2000-11-17  
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;; PRIOR FILING DATE: 2000-11-17  
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;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,207  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,245  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,244  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,217  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,211  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,215  
;; PRIOR FILING DATE: 2000-11-17

;; PRIOR APPLICATION NUMBER: 60/249,264  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,214  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/249,297  
;; PRIOR FILING DATE: 2000-11-17  
;; PRIOR APPLICATION NUMBER: 60/232,400  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/231,242  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,081  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/232,080  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,414  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/231,244  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,064  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/233,063  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,397  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,399  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/232,401  
;; PRIOR FILING DATE: 2000-09-14  
;; PRIOR APPLICATION NUMBER: 60/241,808  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,826  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,786  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/241,221  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/246,475  
;; PRIOR FILING DATE: 2000-11-08  
;; PRIOR APPLICATION NUMBER: 60/231,243  
;; PRIOR FILING DATE: 2000-09-08  
;; PRIOR APPLICATION NUMBER: 60/233,065

Query Match 62.4%; Score 256.4; DB 6; Length 1712;  
Best Local Similarity 79.0%; Pred. No. 1.2e-55;  
Matches 343; Conservative 0; Mismatches 61; Indels 30; Gaps 2;  
  
QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTGAAGGTTGCCAGTGTGAG 60  
|||||  
Db 66 atggagtttgggctgagctgggttttccctgtgtgtgttttaaaagggtgccagtgtag 125  
  
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTCTGG 120  
|||||  
Db 126 gtgcagctggtgagtcctggggagggcttagttcagcctgggggttccctgagactctcc 185  
  
QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATACTACATGACTGGGTCGCCAG 180  
|||||  
Db 186 tgtgcagcgcgtg-----aattcgcccttaagtaactagtgatgcactgggtcccgccaa 239  
  
QY 181 GPTCCAGGCGGCTGGAGTGGGTCTCAGCTATAGTAGTGGTGATCCCATG 240  
|||||  
Db 240 gptccagggaagggtgctatggtctcacatcttaatagtgatggaagtccacaagg 299  
  
QY 241 TAGCGAGACTCCGTGAAGGCGCATTCACCATCTCCAGAGAGAACGCCAACACACTG 300  
|||||  
Db 300 tagcgagactccgtgaaggcgcatcaccatttccagagacacgtccaagaacacactt 359  
  
QY 301 TTTCCTCAATGAACGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA---- 355  
|||||  
Db 360 tatctgcaaatgagcagtcgtgagagtcgagagcacagcgtctcattacgtgtagagga 419  
  
QY 356 -----GCTTACTACAGGGTCTGACTCTCTGGGGCCGAGGAGTCCCTG 396  
|||||  
Db 420 gtaaaagactggcagtagtgggttagccctgactttgactactggtggccagggaacccgtg 479

QY 397 GTACACGGTCTCTCTC 410  
|||||  
Db 480 gtacacgctctctc 493

RESULT 12  
US-10-153-382-1  
; Sequence 1, Application US/10153382  
; GENERAL INFORMATION:  
; APPLICANT: PFIZER PRODUCTS INC.  
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
; FILE REFERENCE: PC23019A  
; CURRENT APPLICATION NUMBER: US/10/153,382  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293042  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1392  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-153-382-1

Query Match 61.9%; Score 254.6; DB 7; Length 1392;  
Best Local Similarity 79.4%; Pred. No. 3.3e-55;  
Matches 331; Conservative 0; Mismatches 74; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTGAAGGTTGCCAGTGTGAG 60  
|||||  
Db 1 atggagtttgggctgagctgggttttccctgtgtgtcttttaagaggtgtccagtgtag 60  
  
QY 61 GTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTCCTGAGACTCTGG 120  
|||||  
Db 61 gtgcagctggtgagctggggagggcggtgccagccctgggaggtccctgagactctcc 120  
  
QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATACTACATGACTGGGTCGCCAG 180  
|||||  
Db 121 tgtgtagcgtctg-----gattcaccttcagtagccatggcagctgggtccgcca 174  
  
QY 181 GTCCAGGCGAGGGGCTGGAGTGGGTCTCAGGTATTAGTAGTGGTGATCCCATG 240  
|||||  
Db 175 gtccaggcgaagggtgagtggtggtggtggtggtggtggtggtggtggtggtggtggt 234  
  
QY 241 TAGCGAGACTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACGCCAACACACTG 300  
|||||  
Db 235 tatgcagactccgtggaaggccgattccaccatctccagagacaaattccaagaacagcgtg 294  
  
QY 301 TTTCCTCAATGAACGCTGAGAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360  
|||||  
Db 295 ttctgcaaatgaacagcgtgagagcgcgagacacggtgtgtattactgtgtagagga 354  
  
QY 361 ACT-----ACAGGGTCTGACTCTCTGGGGCAGGAGTCTGTGTCACCGTCTCTCA 411  
|||||  
Db 355 ggtcaactcggctctttgactactggtggccagggaacccctgggtcaccgtctctctca 411

RESULT 13  
US-10-153-382-4  
; Sequence 4, Application US/10153382  
; GENERAL INFORMATION:  
; APPLICANT: PFIZER PRODUCTS INC.  
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES  
; FILE REFERENCE: PC23019A  
; CURRENT APPLICATION NUMBER: US/10/153,382  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293042  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4

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; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-4

Query Match      61.9%; Score 254.6; DB 7; Length 1392;
Best Local Similarity 79.4%; Pred. No. 3.4e-55;
Matches 331; Conservative 0; Mismatches 74; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTTCCTTGTTCCTCTTTTGAAGAGGTGCCAGTGTGAG 60
Db 1 atggagtttgggctgagctgggttttctctcgttgcctcttcttcttcttcttcttctcag 60

QY 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGCGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgagtgctggggcgctgtgtccagcctgggaggtccctgagactctcc 120

QY 121 TGGCAGCCTCCGGGTTTCAGGTTACACTTCCAATAACTACTACATGAGTGGGTCCGCCAG 180
Db 121 tgtctagcgtctg-----gattcaccttcagtagccatgagcagctgggtcccgccag 174

QY 181 GCTCCAGGCGAGGCGCTGGAGTGGGTCTCACGTATTAGTAGTGGGTGATCCACATGG 240
Db 175 gctccaggccaagggtcggagtcgggtggcagttatagttatgtaTgaggaataataac 234

QY 241 TACGAGACTCCGTTGAAGGGCAGATTTCACCATCTCCAGAGAACGCCAACACACTG 300
Db 235 tatgagagactccgtgaaggccgattccacatctccagagacaattccaagaacacgctg 294

QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
Db 295 ttctcgcaaatgaacagcctgagagccgaggaagcgtgtgtaTctatctgtcgagagga 354

QY 361 ACT-----ACAGGGTCTGACTCTCCCTGGGCCAGGAGTCTCGTCCAGCTCTCCCTCA 411
Db 355 ggtcaacttcgggtccctttgactactcgtgggccaagggaacctggtcacgctctctca 411

RESULT 15
US-10-153-382-8
; Sequence 8, Application US/10153382
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1395
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-8

Query Match      61.6%; Score 253.2; DB 7; Length 1395;
Best Local Similarity 79.0%; Pred. No. 7.6e-55;
Matches 332; Conservative 0; Mismatches 75; Indels 15; Gaps

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTTCCTTGTTCCTCTTTTGAAGAGGTGCCAGTGTGAG 60
Db 1 atggagtttgggctgagctgggttttctctcgttgcctcttcttcttcttcttctcagtgctcag 60

QY 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTTGGCAAGCCTTTGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgagtgctggggcgctgtgtccagcctgggaggtccctgagactctcc 120

QY 121 TGGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACTACTACATGAGTGGGTCCGCCAG 180
Db 121 tgtacagcgtctg-----gattcaccttcagtaactatggatcactcgtgggtcccgccag 174

QY 181 GCTCCAGGCGAGGCGCTGGAGTGGGTCTCACGTATTAGTAGTGGGTGATCCACATGG 240
Db 175 gctccaggccaagggtcggagtcgggtggcagttatagttatgtaTggaagtaataaacac 234

QY 241 TACGAGACTCCGTTGAAGGGCAGATTTCACCATCTCCAGAGAACGCCAACACACTG 300
Db 235 tatgagagactccgtgaaggccgattccacatctccagtgacaaTtccaagaacacgctg 294

QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 353
Db 295 tatctgcaaatgaacagcctgagagccgagggacacggtgtgtatctatctgtcgagagga 354

QY 354 --GAGCTTGACTACAGGGTCTGACTCTCCCTGGGCCAGGAGTCTCGTCCAGCTCTCCCTCA 411
Db 355 gagagactcggggtcctactcttgactactcgtgggccaagggaacctcgtcaccgtctccctca 414

RESULT 14
US-10-153-382-2
; Sequence 2, Application US/10153382
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-2

Query Match      61.9%; Score 254.6; DB 7; Length 1999;
Best Local Similarity 79.4%; Pred. No. 3.4e-55;
Matches 331; Conservative 0; Mismatches 74; Indels 12; Gaps 2;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTTCCTTGTTCCTCTTTTGAAGAGGTGCCAGTGTGAG 60
Db 1 atggagtttgggctgagctgggttttctctcgttgcctcttcttcttcttcttctcagtgctcag 60

QY 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGCGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120
Db 61 gtgcagctgtgagtgctggggcgctgtgtccagcctgggaggtccctgagactctcc 120

QY 121 TGGCAGCCTCCGGGTTTCAGGTTACACTTCCAATAACTACTACATGAGTGGGTCCGCCAG 180
Db 121 gttcagactcgtcgtgagctgggttttctctcgttgcctcttcttcttcttcttctcagtgctcag 174

QY 181 GCTCCAGGCGAGGCGCTGGAGTGGGTCTCACGTATTAGTAGTGGGTGATCCACATGG 240
Db 175 gctccaggccaagggtcggagtcgggtggcagttatagttatgtaTctatctgtcgagagga 354

QY 361 ACT-----ACAGGGTCTGACTCTCCCTGGGCCAGGAGTCTCGTCCAGCTCTCCCTCA 411
Db 355 ggtcaacttcgggtccctttgactactcgtgggccaagggaacctggtcacgctctctca 411

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Search completed: September 23, 2002, 19:58:58  
Job time: 7188 sec

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1



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 18:00:53 ; Search time 110.65 Seconds  
(Without alignments)  
912.385 Million cell updates/sec

Title: US-09-019-441-4  
Perfect score: 411  
Sequence: 1 ATGGAGTTTGGGTGACGTG.....TCCTGGTCACCGTCTCTCA 411

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PTCUTS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	411	100.0	411	3	US-08-803-085-4
2	259.8	63.2	432	1	US-08-026-320A-1
3	252.2	61.4	393	1	US-08-259-372A-3
4	252.2	61.4	393	1	US-08-468-671-3
5	241.8	58.8	423	1	US-08-259-372A-1
6	241.8	58.8	423	1	US-08-468-671-1
7	236.2	57.5	519	3	US-08-545-809A-21
8	236.2	57.5	743	3	US-08-545-809A-48
9	235.6	57.3	715	3	US-08-545-809A-11
10	231.8	56.4	417	4	US-08-134-346A-49
11	227.6	55.4	514	3	US-08-545-809A-23
12	225.8	54.9	405	4	US-08-619-491-7
13	225.8	54.9	405	5	PCT-US95-07302-7
14	225.2	54.8	426	1	US-08-305-683A-1
15	224.2	54.5	1572	3	US-09-049-672A-18
16	223.4	54.4	649	3	US-08-545-809A-64
17	222.4	54.1	413	1	US-08-253-877C-56
18	222.4	54.1	413	2	US-08-452-164A-56
19	222	54.0	418	1	US-07-977-696C-27
20	222	54.0	418	1	US-08-129-930B-27
21	222	54.0	418	4	US-08-976-288A-27
22	221.4	53.9	543	4	US-08-862-124-1
23	221.4	53.9	543	4	US-08-862-124-3
24	220.8	53.7	908	4	US-09-273-839A-9
25	220.6	53.7	354	2	US-08-652-816A-21
26	220	53.5	354	2	US-08-652-816A-22
27	219.2	53.3	348	2	US-08-652-816A-24

28	218.8	53.2	474	2	US-08-653-402B-5	Sequence 5, Appli
29	218.6	53.2	724	3	US-08-545-809A-53	Sequence 53, Appl
30	217.2	52.8	423	2	US-08-646-367-1	Sequence 1, Appli
31	217	52.8	514	3	US-08-545-809A-20	Sequence 20, Appl
32	216.4	52.7	445	1	US-08-053-171-10	Sequence 10, Appl
33	216.4	52.7	491	1	US-08-053-171-6	Sequence 6, Appli
34	216.2	52.6	405	4	US-08-619-491-3	Sequence 3, Appli
35	216.2	52.6	405	5	PCT-US95-07302-3	Sequence 3, Appli
36	216	52.6	405	4	US-08-579-378A-19	Sequence 19, Appl
37	215.6	52.5	892	4	US-09-273-839A-11	Sequence 11, Appl
38	214.4	52.2	640	3	US-08-545-809A-9	Sequence 9, Appli
39	214.2	52.1	1576	1	US-08-157-101A-6	Sequence 6, Appli
40	213.8	52.0	512	3	US-08-545-809A-30	Sequence 30, Appl
41	212.4	51.7	474	2	US-08-653-402B-9	Sequence 9, Appli
42	212.2	51.6	351	2	US-08-428-197-35	Sequence 35, Appl
43	212.2	51.6	351	5	PCT-US93-10555-35	Sequence 35, Appl
44	211.8	51.5	424	2	US-08-765-783A-62	Sequence 62, Appl
45	211.8	51.5	424	3	US-08-921-100-62	Sequence 62, Appl

## ALIGNMENTS

RESULT 1  
US-08-803-085-4  
; Sequence 4, Application US/08803085  
; Patent No. 601138  
; GENERAL INFORMATION:  
; APPLICANT: REFF, Mitchell E.  
; APPLICANT: KLOETZER, William S.  
; APPLICANT: NAKAMURA, Takehiko  
; TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/803,085  
; FILING DATE: 20-FEB-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-353  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 411 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..411  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 58..411  
US-08-803-085-4

Query Match	100.0%;	Score 411;	DB 3;	Length 411;
Best Local Similarity	100.0%;	Pred. No. 4.6e-112;		
Matches 411;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGAGTTTGGGCTGACCTGGGTTTTCTCTGCTTCCTCTTTTAAAGGTGTCACAGTGTGAG	60	
DB	1	ATGGAGTTTGGGCTGACCTGGGTTTTCTCTGCTTCCTCTTTTAAAGGTGTCACAGTGTGAG	60	
QY	61	GTCCAGCTGTGTGAGTCTGGGGCGGCTTGSCAAAGCCTGGGGGTCCTCGAGACTCTGG	120	
DB	61	GTCCAGCTGTGTGAGTCTGGGGCGGCTTGSCAAAGCCTGGGGGTCCTCGAGACTCTGG	120	
QY	121	TGGCAGCCTCCGGTTTCAGGTTTCACCTTCAATTAACACTACATGGACTGGTCCGCCAG	180	
DB	121	TGGCAGCCTCCGGTTTCAGGTTTCACCTTCAATTAACACTACATGGACTGGTCCGCCAG	180	
QY	181	GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCACACATGG	240	
DB	181	GCTCCAGGGCAGGGCTGGAGTGGGTCTCAGTATTAGTAGTGGTGTATCCACACATGG	240	
QY	241	TACGCAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAAAGCCACACACACTG	300	
DB	241	TACGCAGACTCCGTGAAGGCGAGATTCCACCATCTCCAGAGAAAGCCACACACACTG	300	
QY	301	TTTCTTCAAAATGAACGCCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCCAGTTG	360	
DB	301	TTTCTTCAAAATGAACGCCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCCAGTTG	360	
QY	361	ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCTGTGTCACCGTCTCCTCA	411	
DB	361	ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCTGTGTCACCGTCTCCTCA	411	

## RESULT

RESULT 2  
US-08-026-320A-1  
; Sequence 1, Application US/08026320A

PATENT NO. 54139504  
 GENERAL INFORMATION:  
 APPLICANT: Irie, Reiko F  
 TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE  
 NUMBER OF INVENTIONS: 1  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Poms, Smith, Lande & Rose  
 STREET: 2029 Century Park East, Suite 3800  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: United States of America  
 ZIP: 90067

```

1 ZIP: 30007
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: WordPerfect 5.1
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/026,320A
16
17 FILING DATE: 26-FEB-1993
18
19
20

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CLASSIFICATION: 424  
PRIOR APPLICATION DATA: US 07/609803  
APPLICATION NUMBER: 05-NOV-1990  
FILING DATE: 05-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Oldenkamp, David J  
REGISTRATION NUMBER: 29421  
REFERENCE/DOCKET NUMBER: 94268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3107785046  
TELEFAX: 3102771297

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; INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 432 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single

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Query Match	63.2%	Score 259.8;	DB 1;	Length 432;
Best Local Similarity	79.9%;	Pred. NO. 1.5e-67;		
Matches 338;	Conservative	0;	Mismatches 67;	Indels 18;
				Gaps 2;

### RESULTS

RESULTS 3  
US-08-259-372A-3  
; Sequence 3, Application US/08259372A

```
Patent No. 5565354
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: ZM1-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..393
US-08-259-372A-3

Query Match 61.4%; Score 252.2; DB 1; Length 393;
Best Local Similarity 81.5%; Pred. No. 2.6e-65;
Matches 335; Conservative 0; Mismatches 58; Indels 18; Gaps 3;

QY 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTTCCCTTTGAAAGGTGCCAGTGTGAG 60
DB 1 ATGGAGTTGGGCTGAGCTGGGTTTCCCTGTTCCCTTTGAAAGGTGCCAGTGTGAG 60

Patent No. 5565354
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: ZM1-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..393
US-08-259-372A-3

QY 61 GTGACAGCTGGTGGAGTCTGGGGGCGGCTTTGGCAAAAGCCTGGGGGGTCCCTGAGACTCTCTGG 120
DB 61 GTGACAGCTGGTGGAGTCTGGGGGCGGCTTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCTGG 120
QY 121 TGGCGAGCCTCCGGGTTGAGTTCACCTTCAATAACTACTACTAGTGGTGGTCCGCCAG 180
DB 121 TGTGACAGCTCTG-----GATTCACCTTCAGTAGGTAGACATGTGAGTGGGTCCGCCAA 174
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCACGTATTAGTAGTGGTGGTATCCACATGG 240
DB 175 GCTACAGGAAAGGCTGCGAGTGGGTCTCAGCTATTGGTCTTACTGTGA---CACATAC 231
QY 241 TAGGACAGCTCCGTGAAGGCGAGATTTCACCATCTCCAGAGAACGCCAACACACTGG 300
DB 232 TATGACAGACTCCGTGAAGGCGGATTTCACCATCTCCAGAGAAAATGCCAAGAACTCTCTTG 291
QY 301 TTTCTTCAATAAGACAGCCTGAGAGCTGAGAGCTGAGGACACGCTGTCTATTACTGTGGAGCTTG 360
DB 292 TATCTTACAATAAGACGCTGAGAGCGGGGACACGCGCTGTGTATTACTGTGGAAG---- 347
QY 361 ACTACAGGCTCTGACTCTCTGGGCGGAGGAGTCTGCTGATCCAGCTCTCTCA 411
DB 348 -----AGATTAGAACTCTGGGCGGAGGAAACCTTGTCACCGTCTCTCTCA 393

RESULT 4
US-08-468-671-3
Sequence 3, Application US/08468671
Patent No. 5648077
GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
```

REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-50-7  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 393 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: Hybridoma  
CELL LINE: ZM1-1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..393  
US-08-468-671-3

Query Match 61.4%; Score 252.2; DB 1; Length 393;  
Best Local Similarity 81.5%; Pred. No. 2.6e-65;  
Matches 335; Conservative 0; Mismatches 58; Indels 18; Gaps 3;

QY 1 ATGGAGCTTTGGGCTGAGCTGGGTTTCCCTGTCTCTTTTGAAGGTGCCAGTGTGAG 60  
DB 1 ATGGAGCTTTGGGCTGAGCTGGGTTTCCCTGTCTCTTTTGAAGGTGCCAGTGTGAG 60  
QY 61 GTCCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTTGAGACTCTGG 120  
DB 61 GTCCAGCTGGTGGAGTCTGGGGCGGCTTGGTACACCTGGGGGTCCTTGAGACTCTCC 120  
QY 121 TGGCGAGCTCCGGGTTGAGTTCACCTTCAATACTACTAGTACGTGGGTCCGCCAG 180  
DB 121 TGTGACAGCTCTG-----GATTACCTTCAGTAGTAGCATGTACTGGGTCCGCCAA 174  
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGCATCCACATGG 240  
DB 175 GCTACAGGAAGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGCATCCACATAC 231  
QY 241 TAGCGAGCTCCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300  
DB 232 TATGCAGACTCCGTGAAGGCGGATTACCATCTCCAGAGAGAAATGCCAAGAACTCCTG 291  
QY 301 TTCTTCAATGAACAGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGGAGCTTG 360  
DB 292 TATCTTACAATGAACGCTGAGAGCGGGGACACGGCTGTCTATTACTGTGCAAG---- 347  
QY 361 ACTACAGGCTGTACTCTCTGGGCGAGGAGTCTGGTCAACGCTCTCTCA 411  
DB 348 -----AGATTGAACTCTGGGCGCAGGGAACCCCTGGTCAACGCTCTCTCA 393

RESULT 5  
US-08-259-372A-1

Sequence 1, Application US/08259372A

Patent No. 5565354

GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.

TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,372A  
FILING DATE: 14-JUN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/871,426  
FILING DATE: 21-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,036  
FILING DATE: 27-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/538,796  
FILING DATE: 15-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/192,754  
FILING DATE: 11-MAY-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/925,196  
FILING DATE: 31-OCT-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 06/904,517  
FILING DATE: 05-SEP-1986  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-50-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: Hybridoma  
CELL LINE: PE1-1  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..423  
US-08-259-372A-1

Query Match 58.8%; Score 241.8; DB 1; Length 423;  
Best Local Similarity 82.3%; Pred. No. 3e-62;

Matches 292; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTCTCTTTTGAAGGTGCCAGTGTGAG 60  
DB 1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTCTCTTTTGAAGGTGCCAGTGTGAG 60  
QY 61 GTCCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTGGGGGTCCTTGAGACTCTGG 120  
DB 61 GTCCAGCTGGTGGAGTCTGGGGCGGCTTGGTACACCTGGGGGTCCTTGAGACTCTCC 120  
QY 121 TGGCGAGCTCCGGGTTGAGTTCACCTTCAATACTACTAGTACGTGGGTCCGCCAG 180  
DB 121 TGTGAGCCTCTG-----GATTACCTTCAGTAGTAGCATGTACTGGGTCCGCCAG 174  
QY 181 GCTCCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGGTGCATCCACATGG 240  
DB 175 GCTCCAGGCGAGGGCTGGAGTGGGTGGCGATCATCATATGATGGAAGTAATAATGG 234

QY 241 TAGCAGACTCGTGAAGGCGAGATTCCACCTCCAGAGAGAACCCCAACACACTG 300  
Db 235 TAGCAGACTCGTGAAGGCGAGATTCCACCTCCAGAGAGAACCCCAACACACTG 294  
QY 301 TTCTTCAAAATGAACGCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 355  
Db 295 TTCTGCAAAATGCACAGCTGAGAGCTGCGGACACGGGTGTATATCTGTGCGA 349

## RESULT 6

US-08-468-671-1

; Sequence 1, Application US/08468671

; Patent No. 5648077

; GENERAL INFORMATION:

; APPLICANT: Ostberg, Lars G.

; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,671

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/259,372

; FILING DATE: 14-JUN-1994

; APPLICATION NUMBER: US 07/871,426

; FILING DATE: 21-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/676,036

; FILING DATE: 27-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/538,796

; FILING DATE: 15-JUN-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/192,754

; FILING DATE: 11-MAY-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 06/925,196

; FILING DATE: 31-OCT-1986

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 06/904,517

; FILING DATE: 05-SEP-1986

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-50-7

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 423 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; CELL TYPE: Hybridoma

; CELL LINE: PE1-1  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..423  
US-08-468-671-1

Query Match 58.8%; Score 241.8; DB 1; Length 423;

Best Local Similarity 82.3%; Pred. No. 3e-62;

Matches 292; Conservative 0; Mismatches 57; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTTCCCTGTTCCCTCTTTTGAAGAGTGTGCCAGTGTGAG 60

Db 1 ATGGAGTTTGGGCTGAGCTGGGTTTTTCCCTGTTCCCTCTTTTGAAGAGTGTGCCAGTGTGAG 60

QY 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAAAGCCTGGGGGGTCCCTGAGACTCTGG 120

Db 61 GTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAAAGCCTGGGGGGTCCCTGAGACTCTGG 120

QY 121 TCGGAGCCTCGGGTTCAGGTTTCAGCTTCACTTCAATACTACTAGTGGTGGTCCGCCAG 180

Db 121 TGTGCAGCCTCTG-----GATTCACCTTCAGTAGGTATGGCATGCACTGGGTCCGCCAG 174

QY 181 GCTCCAGGCGAGGGGCTGGAGTGGGTCTCAGCTATTAGTAGTGTGATCCACATGG 240

Db 175 GCTCCAGGCGAGGGGCTGGAGTGGGTGGCAGTATCATATGTAAGTAATAATGG 234

QY 241 TAGCAGACTCCGTGAAGGCGAGATTCCACCTATCTCCAGAGAGAACGCCAACACACTG 300

Db 235 TATGCAGACTCCGTGAAGGCGGATTCCACCTATCTCCAGAGAGAACATCCCAAGAACTCTG 294

QY 301 TTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA 355

Db 295 TTCTGCAAAATGCACAGCTGAGAGCTGCGGACACGGGTGTATATCTGTGCGA 349

## RESULT 7

US-08-545-809A-21

; Sequence 21, Application US/08545809A

; Patent No. 6096878

; GENERAL INFORMATION:

; APPLICANT: Honjo, Tasuku

; APPLICANT: Matsuda, Fumihiko

; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 145

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish &amp; Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/545,809A

; FILING DATE: 27-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP93/00603

; FILING DATE: 10-MAY-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 06501/004001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:  
LENGTH: 519 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: human lymphoblast  
CELL LINE: CGM1  
US-08-545-809A-21

Query Match 57.5%; Score 236.2; DB 3; Length 519;  
Best Local Similarity 85.0%; Pred. No. 1.5e-60;  
Matches 278; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 30 TGTTCCTCTTTTGAAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 89  
DB 141 TGTCTCTCTGTTTGCAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 200  
QY 90 GCAAGAGCTGGGGTCCCTCAGACTCTGTTGCGCAGCTCCGGGTTTCAGGTTACCTT 149  
DB 201 GGTCAAGCTGGGGTCCCTCAGACTCTCTCTGTCAGGCTCTG-----GATTCACCTT 254  
QY 150 CAATAACTACTACATGAGTGGTCCGCCAGGCTCCAGGCGAGGGCTGGAGTGGGTCTC 209  
DB 255 CAGTAGCTATAGCATGAATCGGTCCGCCAGGCTCCAGGAGGGCTGGAGTGGGTCTC 314  
QY 210 AGCTATTAGTAGTGGTGATCCACATGTTACGAGACTCCGTTGAAGGGCAGATTTCAC 269  
DB 315 ATCCATTAGTAGTAGTGGTGATCCACATGTTACATATACGAGACTCAGTGAAGGGCGATTTCAC 374  
QY 270 CATCTCCAGAGAGAGCGCCCAACACACTGTTCTTCAAAATGAACAGCTCAGAGCTCA 329  
DB 375 CATCTCCAGAGAGAGCGCCCAACACACTGTTCTTCAAAATGAACAGCTCAGAGCTCA 434  
QY 330 GGACAGGCTGTCTATTACTGTGCGAG 356  
DB 435 GGACAGGCTGTGTATTACTGTGCGAG 461

## RESULT 8

US-08-545-809A-48  
Sequence 48, Application US/08545809A  
Patent No. 6096878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 743 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: human lymphoblast  
CELL LINE: CGM1  
US-08-545-809A-48

Query Match 57.5%; Score 236.2; DB 3; Length 743;  
Best Local Similarity 85.0%; Pred. No. 1.7e-60;  
Matches 278; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

QY 30 TGTTCCTCTTTTGAAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 89  
DB 306 TGTCTCTCTGTTTGCAGGTGTCAGGTGAGGTGAGTGCAGTGTGGGGGGGGCTT 365  
QY 90 GCAAGAGCTGGGGTCCCTCAGACTCTGTTGCGCAGCTCCGGGTTTCAGGTTACCTT 149  
DB 366 GTTACAGCTGGGGTCCCTCAGACTCTCTCTGTCAGGCTCTG-----GATTCACCTT 419  
QY 150 CAATAACTACTACATGAGTGGTCCGCCAGGCTCCAGGCGAGGGCTGGAGTGGGTCTC 209  
DB 420 CAGTAGCTATAGCATGAATCGGTCCGCCAGGCTCCAGGAGGGCTGGAGTGGGTCTC 479  
QY 210 AGCTATTAGTAGTGGTGATCCACATGTTACGAGACTCCGTTGAAGGGCAGATTTCAC 269  
DB 480 ATACATTAGTAGTAGTGGTGATCCATATACGAGACTCTGTGAAGGGCGGATTTCAC 539  
QY 270 CATCTCCAGAGAGAGCGCCCAACACACTGTTCTTCAAAATGAACAGCTCAGAGCTCA 329  
DB 540 CATCTCCAGAGAGAGCGCCCAACACACTGTTCTTCAAAATGAACAGCTCAGAGCTCA 599  
QY 330 GGACAGGCTGTCTATTACTGTGCGAG 356  
DB 600 GGACAGGCTGTGTATTACTGTGCGAG 626

## RESULT 9

US-08-545-809A-11  
Sequence 11, Application US/08545809A  
Patent No. 6096878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP93/00603
: FILING DATE: 10-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Freeman, John W.
: REGISTRATION NUMBER: 29,066
: REFERENCE/DOCKET NUMBER: 06501/004001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-542-5070
: TELEFAX: 617-542-8906
: TELEX: 200134
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 715 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: Genomic DNA
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: human lymphoblast
: CGML
: US-08-545-809A-11

```

Query Match	57.3%	Score 235.6;	DB 3;	Length 715;
Best Local Similarity	84.8%;	Pred. No. 2.5e-60;		
Matches 278;	Conservative 0;	Mismatches 44;	Indels 6;	Gaps 1;

  

QY	29	TTGTTCTCTCTTTTCAAAGGTGTC	CCAGTGT	CAGGTGC	AGCTG	TGGTGA	CTCTGGGGCGCGCT	88
Db	331	TTGTTCTCTGTTTTCAGAGTGT	CCAGTGT	CAGGTGC	AGCTG	TGGTGA	CTCTGGGGGAGGCT	390
QY	89	TGSCAAAGCCTGGGGGTCCTCCT	GAGACTCT	TGGTCG	CAGCCT	CCGGGTT	CAGGTTCA	148
Db	391	TGGTCAGCCTGGAGGTCCTCCT	GAGACTCT	CTCTGT	GCAGCCT	CTG-----	GATTCACT	444
QY	149	TCAATACTACTACATGGACTGGG	TCCG	CAGGCT	TCCAGGC	AGGGCT	CTGGAGTGGTCT	208
Db	445	TCAGTGACTACTACATGAGCTGG	ATCCG	CAGGCT	TCCAGGA	AGGGCT	CTGGAGTGGGTTT	504
QY	209	CACGTATTACTAGTAGTGGTGAT	CCCA	CACATGGT	TACG	CAGACT	CCGTTCAAGGCGAGATTCA	268
Db	505	CATACATTAGTAGTGGTAGTACC	ATAT	ACTACG	CAGACT	CTGTGA	AGGGCGGAGATTCA	564
QY	269	CCATCTCCAGAGAGACGCCCAAC	AACACT	GTGTTCT	TTC	CAAAAT	GAACAGCCTGAGAGCTG	328
Db	565	CCATCTCCAGGACAGGCCCAAG	CACT	GTATCT	GTCAAT	TGAAC	AGCCTGAGAGCCG	624
QY	329	AGGACAGCGGTGCTATTACTGT	CGGAG					356
Db	625	AGGACAGCGCGGTGATTACTGT	CGGAG					652

```

RESULT 10
US-08-134-346A-49
; Sequence 49, Application US/08134346A
; Patent No. 6281335
; GENERAL INVENTION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,346A
FILING DATE: 08-OCT-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Onofrio, Dara L.
REGISTRATION NUMBER: 34,889
REFERENCE/DOCKET NUMBER: CLT 149,608
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-826-6565
TELEFAX: 212-826-5909
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-134-346A-49

```

Query Match	56.4%;	Score	231.8;	DB	4;	Length	417;
Best Local Similarity	76.1%;	Pred. No.	2.6e-59;				
Matches	319;	Conservative	0;	Mismatches	82;	Indels	18;
Gaps	2;						

  

QY	1	ATGAGATTGGCGTGCAGCTGGGTTTCTCTTGTTCTCTTTTAAAGGTGTCAGTGTGAG	60
DB			
	1	ATGCACTTTGGGCTCAGCTTGGTTTTCTTCTTGCTTAATTTAAAGGTGCCAGTGTGAA	60
QY	61	GTCCAGCTGTGTGAGTCTGGGGCGGCTTGCAGAAAGCTTGGGGGTCCCTGAGACTCTGG	120
DB			
	61	GTCCAGATGTGTGAGTCTGGGGAGGCTTGTAGTCAGCTGTGAGGCTCCCTGAGACTCTCC	120
QY	121	TGCGCAGCCTCCGGGTTTCAGGTTCACTTCACTCAATAAATCTACATGGACTGGTCCGCCAG	180
DB			
	121	TGTGCAAGCTCTG-----GATTGCGTTTCTCAGTAGCTATGCCATGCTTGGGTTTCGCCAG	174
QY	181	GTCCAGGCGAGGGGCTGGAGTGGGTTCTCAGTATTAGTAGTGTGTGATCCACACTGG	240
DB			
	175	GCTCCAGGAAGGGCTGGAGTGGTTCGAGAAATTAGTAGTGTGTGTAATTACGCCTAC	234
QY	241	TAGCAGACTCGGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCACACACACTG	300
DB			
	235	TATCAAGACACTGTGACGGCCGAGTTACCATCTCCAGAGACAAATCCCAAGAACCCCTG	294
QY	301	TTTCTTCAAAATGAACGCTTGAGACGTGAGSACACGCTGTCTATTACTGTGTGCA-----	355
DB			
	295	TACCTGCAATGAACAGCTCTGAGGGCTGAGGACACGGCCGTGTATTACTGTGCAAGGGAG	354
QY	356	-----GCTTGACTACAGGGCTGTGACTCTCTGGGGCCAGGGAGTCTTGTCACCGTCTC	407
DB			
	355	GACTACGGTATCCCGGCTGTGGTTGCTTACTTGGGGCCAAAGGACTCTGGTCACTGTCTC	413

RESULT 11  
US-08-545-809A-23  
; Sequence 23, Application US/08545809A  
; Patent No. 6096878  
; GENERAL INFORMATION:  
; APPLICANT: Honjo, Tasuku  
; APPLICANT: Matsuda, Fumihiko  
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE  
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
; NUMBER OF SEQUENCES: 145  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston

STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 514 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
CELL TYPE: human lymphoblast  
CELL LINE: CGMI  
US-08-545-809A-23

Query Match 55.4%; Score 227.6; DB 3; Length 514;  
Best Local Similarity 84.4%; Pred. No. 4.9e-58;  
Matches 270; Conservative 0; Mismatches 44; Indels 6; Gaps 1;

QY 36 TCCTTTTGAAGGTGTCAGGTGAGTGCAGTGTGGAGTCTGGGGGGGCTTGCAAA 95  
DB 148 TTTGTTTGCAGGTGTCAGGTGAGTGCAGTGTGGAGTCTGGGGGGGCTTGCTACA 207  
QY 96 GCTGTGGGGTCCCTCAGACTCTGCTGGCGAGGCTCCGGTTCAGGTTCACCTTCAATTA 155  
DB 208 GCCTGGGGGTCCCTCAGACTCTCCTGTGCAGCCTCTG-----GATTCACCTTTAGCAG 261  
QY 156 CTACTACATGAGTGGGTCCGGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTCAGGTAT 215  
DB 262 CTATGCCATGAGTGGGTCCGGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTAT 321  
QY 216 TAGTAGTGTGTGATCCACATGTTACGAGACTCCGTGAAGGGCAGATTCACCATCTC 275  
DB 322 TAGTGTGTGTGTGTGATCCACATGTTACGAGACTCCGTGAAGGGCAGATTCACCATCTC 381  
QY 276 CAGAGAGACGCCCAACACACTGTTCTTCAATGACAGCCTGAGAGCTGAGGACAC 335  
DB 382 CAGAGACAAATCCAGAACACCTGTATCTGCAATGAACAGCCTGAGAGCGCAGGACAC 441  
QY 336 GGCTGTCTATTACTGTGCGA 355  
DB 442 GGCCGTATATTACTGTGCGA 461

RESULT 12  
US-08-619-491-7  
Sequence 7, Application US/08619491  
Patent No. 6210670  
GENERAL INFORMATION:  
APPLICANT: Berg, Ellen L.  
TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies  
TITLE OF INVENTION: Specific for E-Selectin and p-Selectin

NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/619,491  
FILING DATE: 26-MAR-1996  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US95/07302  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/259,963  
FILING DATE: 14-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 011823-0058100S  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..405  
OTHER INFORMATION: /note= "humanized 5c7.29 antibody heavy  
OTHER INFORMATION: chain variable region synthetic DNA"  
US-08-619-491-7

Query Match 54.9%; Score 225.8; DB 4; Length 405;  
Best Local Similarity 73.7%; Pred. No. 1.5e-57;  
Matches 303; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

QY 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTGTGTCCTTTTGAAGGTGTCCAGTGTGAG 60  
DB 1 ATGGACTCCAGGCTCAATTTAGTTTTCCTTGTCTTATTTAAAGGTGTCCAGTGTGAA 60  
QY 61 GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCCTGGGGGGTCCCTGAGACTCTGG 120  
DB 61 GTACAACTGGTGGAGTCTGGGGGAGGTTAGTGCAGCTGGAGGTCCTTCTCTCTCC 120  
QY 121 TCGCGAGCTCCGGGTTTCAGTTTCACCTTCAATACTACTACATGAGCTGGGTCCGCCAG 180  
DB 121 TGTGAGCCTCTG-----GATTCACCTTTCAGTAGCTTTGGAAATGCACTGGGTCTGAG 174  
QY 181 GCTCAGGCGAGGGCTGGAGTGGGTCTCAGCTATTTAGTAGTGGTGTATCCCATG 240  
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QY 241 TAGCGAGACTCCGTGAGGGCAGATTCCACATCTCCAGAGAACCCCAACACACTG 300  
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QY 361 ACTACAGGCTGACTCCTGGGCGGAGTCTGGTCAACGCTCTCTCA 411  
Db 355 TTACCCCGCTTGTCTACTTGGGGCCAAAGGACTTTGGTCACTGTCTCTCA 405

## RESULT 13

PCT-US95-07302-7  
; Sequence 7, Application PC/TUS9507302  
; GENERAL INFORMATION:  
; APPLICANT: Berg, Ellen L.  
; TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies  
; TITLE OF INVENTION: Specific for E-Selectin and P-Selectin  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/07302  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/259,963  
; FILING DATE: 14-JUNE-94  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-005810PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 405 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..405  
PCT-US95-07302-7

Query Match 54.9%; Score 225.8; DB 5; Length 405;  
Best Local Similarity 73.7%; Pred. No. 1.5e-57;  
Matches 303; Conservative 0; Mismatches 102; Indels 6; Gaps 1;

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QY 181 GCTCCAGGCGAGGGGTGAGTGGGTCTCAAGTATTTAGTAGTGTGATCCACATGG 240  
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Db 235 TATGCTGACACAGTGAAGGGCGGATTCACCATCTCCAGAGACACACAGACACCCCTG 294  
QY 301 TTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360  
Db 295 TATCTGCAAAATGAACAGTCTAAGGGCTGAGGACACGGCGCTGTATTACTGTGCAAGACCT 354  
QY 361 ACTACAGGCTGACTCCTGGGCGGAGGAGTCTGGTCAACGCTCTCTCTCA 411  
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## RESULT 14

US-08-305-683A-1  
; Sequence 1, Application US/08305683A  
; Patent No. 5646041  
; GENERAL INFORMATION:  
; APPLICANT: HARFELDT, Elisabeth  
; APPLICANT: LAKE, Philip  
; APPLICANT: NOTTAGE, Barbara  
; APPLICANT: OSTBERG, Lars G.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX  
; TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/305,683A  
; FILING DATE: 13-SEP-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/759,279  
; FILING DATE: 13-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 11823-005230  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 426 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..426  
; OTHER INFORMATION: /product= "HSV863 heavy chain  
; OTHER INFORMATION: variable region"  
US-08-305-683A-1

Query Match 54.8%; Score 225.2; DB 1; Length 426;  
Best Local Similarity 79.2%; Pred. No. 2.3e-57;  
Matches 282; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

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QY 61 GTGCAGCTGTGGAGTCTGGGGGGGGTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 120  
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QY 121 TGGCAGCTGTGGAGTCTGGGGGGGGTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 180  
Db 121 TGGCAGCTGTGGAGTCTGGGGGGGGTGGCAAGCCTGGGGGGTCCCTGAGACTCTGG 174  
QY 181 GCTCCAGGCAAGGGCTGGAGTGGCTGCTACGATTTAGTAGTAGTGGTATCCACATGG 240  
Db 175 GCTCCAGGCAAGGGCTGGAGTGGCTGCTACGATTTAGTAGTAGTGGTATCCACATGG 234  
QY 241 TAGCCAGACTCCCTGAGGCGAGATTACCATCTCCAGAGAGAACGCCCAACACACTG 300  
Db 235 TAGGAGAGTCCCTGAGGCGCGATTTCATCATCTCCAGAGACAAATCCCAAGATATCCTG 294  
QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACACGCTGTCTATTACTGTGCGAG 356  
Db 295 TATCTGCAATGAACAGCCTGAGAGCGGAGGACACGCGCTGTGTATTACTGTGCGAG 350

## RESULT 15

US-09-049-672A-18  
; Sequence 18, Application US/09049672A  
; Patent No. 6135941

## ; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/049,672A

; FILING DATE: HEREWITH

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0497 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1572 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: BMARNOT03

; CLONING: 1669829

US-09-049-672A-18

Query Match 54.5%; Score 224.2; DB 3; Length 1572;

Best Local Similarity 79.2%; Pred. No. 7.6e-57;

Matches 281; Conservative 0; Mismatches 68; Indels 6; Gaps 1;

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Db 64 ATGGAGTTGGGACTGAGCTGGGTTTTCCTTGTTCCTTTTAAAGGTGTCCAGTGTGAA 123  
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Db 124 GTGCAGCTGTGGAGTCTGGGGGGGGTGGTACAGCCTGGCAGGTCCCTGAGACTCTCC 183  
QY 121 TGGCAGCTCCCGGTTTCAGGTTTCACCTTCAATAACTACTACATGACTGGGTCCGCCAG 180  
Db 184 TGTGCAGCTCTG-----GATTCACCTTTGTGATGCCATGCCATGACTGGGTCCGGCAA 237  
QY 181 GTTCCAGGCGAGGGGCTGGAGTGGGTCTCACGTPATTAGTAGTAGTGGTATCCCATGG 240  
Db 238 ATTCCAGGGAAGGGCTGGAGTGGGTCTCAGGTATTAAATTGGCATAGTGTACCATAGGC 297  
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Db 298 TATGCGAACTCTGTAAAGGGCGGATTTCACCATCTCCAGAGACAAACGCCAAGAGCTCCCTG 357  
QY 301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACACGCTGTCTATTACTGTGCGA 355  
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Job time: 3227 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:50:25 ; Search time 6364.12 Seconds  
(without alignments)  
1325.809 Million cell updates/sec

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Perfect score: 390  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%  
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#### SUMMARIES

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5	330.8	84.8	607	17	US-09-396-885-4438
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9	327.4	83.9	465	17	US-09-359-087-41768
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23	322.8	82.8	508	55	US-60-168-599-294
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25	322.4	82.7	1460	37	US-10-076-747-8
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27	321.2	82.4	379	18	US-09-489-036-8482
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31	321.2	82.4	891	14	US-09-049-672-23





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Db	85	tctgacctgactcagctccctccggtccgggtccctcgacagtcagtcacatctcc	144
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Qy	181	CCAGGCAAAAGCCCCCAAACTCATGATTATGATGTGCTAAGCGGGCCTCAGGGGTCTCT	240
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; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20661
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-287-618-20661

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Best Local Similarity 90.5%;      Pred. No. 1.4e-83;
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QY 121 TGCACCTGGAAACGACGATGACGTTGGTGGTTATTAATCTATGTCTCTGGTACCAACCCAC 180
Db 151 tgcactggaaacacagcagtgacattggtttacaacatgtctcctggtaaccaaacac 210
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Db 331 gctgaggacgaggtgattattactgagctcctacatacaagcagcgatctctggtggtc 390
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Db 391 ggcggagggaaccaagctgacctcctggtc 420
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